

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: September 15, 2005, 18:18:32 ; Search time 204 Seconds
 (without alignments)
 7275.015 Million cell updates/sec

Title: US-09-989-733-398
 Perfect score: 907
 Sequence: 1 ggactctaaaggcccaagc.....gtgagactccatcacaca 907

Scoring table: IDENTITY_NUC
 GapOp 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 1500 summaries

Database : Issued_Patents_NA.*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
 5: /cgn2_6/ptodata/1/ina/PCUTUS_COMB.seq: *
 6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	905.4	99.8	12445	4 US-09-949-016-14632
2	905.4	99.8	21691	4 US-09-949-016-15748
3	601.6	66.3	11549	4 US-09-949-016-2024
4	500	55.1	1500	3 US-09-276-517-73
5	211.8	23.4	167059	4 US-09-949-016-16514
6	211.8	23.3	23533	4 US-09-949-016-15377
7	210.6	23.2	36148	4 US-09-949-016-12969
8	210.6	23.2	64813	4 US-09-949-016-11957
9	210.6	23.2	70131	4 US-09-949-016-16064
10	210.4	23.2	63187	4 US-09-949-016-12682
11	210.4	23.2	63187	4 US-09-949-016-16288
12	209.2	23.1	35678	4 US-09-949-016-12786
13	209.2	23.1	35678	4 US-09-949-016-16757
14	209.2	23.1	35678	4 US-09-949-016-16758
15	209.2	23.1	58361	4 US-09-949-016-16755
16	209.2	23.1	59065	3 US-09-813-817-3
17	209.2	23.1	59065	3 US-09-978-197-3
18	209.2	23.1	59065	4 US-10-135-696-3
19	209.2	23.1	59065	4 US-10-135-696-3
20	209.2	23.1	71815	4 US-09-949-016-12501
21	209	23.0	125672	4 US-09-949-016-16956
22	208.8	23.0	601	4 US-09-949-016-121405
23	208.8	23.0	48691	4 US-09-949-016-16308
24	208.6	23.0	12708	4 US-09-949-016-13216
25	208.4	23.0	601	4 US-09-949-016-16309
26	208.4	23.0	601	4 US-09-949-016-163070
27	208.2	23.0	107941	4 US-09-949-016-14206

28	208.2	23.0	109378	4 US-09-949-016-12391
29	208.2	23.0	16061	4 US-09-949-016-1422
30	207.8	22.9	91701	4 US-09-949-016-14891
31	207.8	22.9	94855	4 US-09-949-016-1264
32	207.8	22.9	19889	4 US-09-949-016-15654
33	207.5	22.9	5886	4 US-09-949-016-15129
34	207.4	22.9	5161	4 US-09-949-016-11905
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53	207.2	22.8	601	4 US-09-949-016-17390
54	207.2	22.8	601	4 US-09-949-016-17931
55	207.2	22.8	601	4 US-09-949-016-30309
56	206.8	22.8	601	4 US-09-949-016-192297
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102	206	22.7	818128	4	US-09-949-016-14565	Sequence 14566, A	C 175	204	22.5	80556	4	US-09-949-016-13064
103	206	22.7	818128	4	US-09-949-016-14567	Sequence 14567, A	C 176	204	22.5	40355	4	US-09-949-016-12715
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105	205.8	22.7	43550	4	US-09-949-016-12400	Sequence 12400, A	C 178	204	22.5	198560	4	US-09-949-016-17202
106	205.8	22.7	43155	4	US-09-949-016-13933	Sequence 13933, A	C 179	204	22.5	421118	4	US-09-949-016-15297
107	205.8	22.7	144956	4	US-09-949-016-11749	Sequence 11749, A	C 180	203.8	22.5	95500	3	US-09-798-096-10
108	205.8	22.7	144956	4	US-09-949-016-13035	Sequence 13035, A	C 181	203.6	22.4	601	4	US-09-949-016-163106
109	205.6	22.7	601	4	US-09-949-016-17835	Sequence 17835, A	C 182	203.5	22.4	25122	4	US-09-949-016-16312
110	205.6	22.7	601	4	US-09-949-016-17075	Sequence 41705, A	C 183	203.6	22.4	15265	4	US-09-949-016-16089
111	205.6	22.7	601	4	US-09-949-016-96560	Sequence 96560, A	C 184	203.4	22.4	194933	4	US-09-949-016-14172
112	205.6	22.7	601	4	US-09-949-016-9826	Sequence 96826, A	C 185	203.4	22.4	601	4	US-09-949-016-13415
113	205.6	22.7	601	4	US-09-949-016-97092	Sequence 97092, A	C 186	203.4	22.4	601	4	US-09-949-016-41050
114	205.6	22.7	601	4	US-09-949-016-97558	Sequence 97358, A	C 187	203.4	22.4	30456	4	US-09-949-016-44213
115	205.6	22.7	601	4	US-09-949-016-97624	Sequence 97624, A	C 188	203.4	22.4	44439	4	US-09-949-016-17102
116	205.6	22.7	601	4	US-09-949-016-97890	Sequence 97890, A	C 189	203.4	22.4	47727	4	US-09-949-016-12904
117	205.6	22.7	601	4	US-09-949-016-98156	Sequence 98156, A	C 190	203.4	22.4	62728	4	US-09-949-016-12539
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124	205.6	22.7	601	4	US-09-949-016-10018	Sequence 10018, A	C 197	203.2	22.4	17884	4	US-09-949-016-13039
125	205.6	22.7	601	4	US-09-949-016-10084	Sequence 10028, A	C 198	203.2	22.4	236474	4	US-09-949-016-17175
126	205.6	22.7	601	4	US-09-949-016-10050	Sequence 100550, A	C 199	203.2	22.4	601	4	US-09-949-016-13418
127	205.6	22.7	601	4	US-09-949-016-10238	Sequence 10238, A	C 200	203.2	22.4	40742	4	US-09-949-016-33417
128	205.6	22.7	601	4	US-09-949-016-10816	Sequence 10816, A	C 201	203	22.4	601	4	US-09-949-016-33418
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133	205.6	22.6	601	4	US-09-949-016-10478	Sequence 10478, A	C 212	203	22.4	601	4	US-09-949-016-17151
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135	205.6	22.6	601	4	US-09-949-016-11273	Sequence 11273, A	C 208	203	22.4	107458	4	US-09-949-016-15457
136	205.6	22.6	601	4	US-09-949-016-15932	Sequence 15932, A	C 214	203	22.4	114793	4	US-10-148-806-3
137	205.6	22.7	193169	4	US-09-949-016-15091	Sequence 15091, A	C 215	203	22.4	123863	4	US-09-949-016-13548
138	205.4	22.6	47784	4	US-09-949-016-15991	Sequence 149191, A	C 216	203	22.4	56241	4	US-09-949-016-15177
139	205.4	22.6	601	4	US-09-949-016-15956	Sequence 149196, A	C 217	203	22.4	56241	4	US-09-949-016-15054
140	205.4	22.6	8345	4	US-09-949-016-16833	Sequence 16833, A	C 218	203	22.4	27607	4	US-09-949-016-15874
141	205.4	22.6	56516	3	US-09-949-016-119486	Sequence 15938, A	C 219	202.8	22.4	40168	4	US-09-949-016-13225
142	205.4	22.6	26552	4	US-09-949-016-12736	Sequence 15939, A	C 220	202.8	22.4	95108	4	US-09-949-016-16681
143	205.4	22.6	42373	4	US-09-949-016-16338	Sequence 16438, A	C 221	202.8	22.4	93518	4	US-09-949-016-14202
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146	205.2	22.6	601	4	US-09-949-016-16833	Sequence 16833, A	C 224	202.6	22.3	601	4	US-09-949-016-15784
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151	204.8	22.6	601	4	US-09-949-016-1641031	Sequence 149190, A	C 229	202.4	22.3	601	4	US-09-949-016-148623
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155	204.8	22.6	7404	4	US-09-949-016-15118	Sequence 15118, A	C 233	202.4	22.3	69763	4	US-09-949-016-12584
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157	204.6	22.6	601	4	US-09-949-016-1641031	Sequence 149190, A	C 235	202.4	22.3	601	4	US-09-949-016-191425
158	204.6	22.6	42354	4	US-09-949-016-16723	Sequence 17123, A	C 236	202.4	22.3	63930	4	US-09-949-016-17229
159	204.6	22.6	42354	4	US-09-949-016-16960	Sequence 17124, A	C 237	202.4	22.3	10690	4	US-09-949-016-16960
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161	204.6	22.6	89550	4	US-09-949-016-17150	Sequence 12935, A	C 239	202.4	22.3	49497	4	US-09-949-016-15316
162	204.4	22.5	10029	4	US-09-949-016-16846	Sequence 11846, A	C 240	202.4	22.3	49497	4	US-09-949-016-13101
163	204.4	22.5	36332	4	US-09-949-016-16245	Sequence 12415, A	C 241	202.2	22.3	9365	3	US-09-608-285A-8
164	204.4	22.5	36333	4	US-09-949-016-15754	Sequence 15754, A	C 242	202.2	22.3	9365	3	US-09-350-836B-8
165	204.4	22.5	404520	4	US-09-949-016-13030	Sequence 13303, A	C 243	202.2	22.3	9365	3	US-09-370-265-B
166	204.4	22.5	42354	4	US-09-949-016-164731	Sequence 14731, A	C 244	202.2	22.3	9365	3	US-09-557-800C-8
167	204.4	22.5	144158	4	US-09-949-016-12916	Sequence 12916, A	C 245	202.2	22.3	9365	4	US-09-949-016-12524
168	204.4	22.5	10029	4	US-09-949-016-16184	Sequence 11846, A	C 246	202.2	22.3	47479	4	US-09-949-016-17590
169	204.4	22.5	36333	4	US-09-949-016-1615754	Sequence 15754, A	C 247	202.2	22.3	9365	3	US-09-449-016-17220
170	204.2	22.5	404520	4	US-09-949-016-16330	Sequence 13303, A	C 248	202.2	22.3	9365	3	US-09-949-016-13525
171	204.2	22.5	42354	4	US-09-949-016-164731	Sequence 14731, A	C 249	202.2	22.3	9365	3	US-09-949-016-12298
172	204.2	22.5	601	4	US-09-949-016-162817	Sequence 12817, A	C 250	202.2	22.3	9365	4	US-09-949-016-15316
173	204	22.5	7561	4	US-09-949-016-11816	Sequence 11816, A	C 251	202.2	22.3	47479	4	US-09-949-016-12524

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C	248	202.2	22.3	15977	3	US-09-608-285A-59	Sequence 16423, A
C	249	202.2	22.3	24593	4	US-09-949-016-13433	Sequence 9, A
C	250	202.2	22.3	30843	4	US-09-949-016-1487	Sequence 9, A
C	251	202.2	22.3	91831	4	US-09-949-016-13684	Sequence 6, A
C	252	202.2	22.3	107800	4	US-09-949-016-13118	Sequence 13694, A
C	253	202.2	22.3	107937	4	US-09-949-016-17192	Sequence 13118, A
C	254	202.2	22.3	11625	4	US-09-949-016-11809	Sequence 17192, A
C	255	202.2	22.3	23552	4	US-09-949-016-13675	Sequence 11809, A
C	256	202	22.3	601	4	US-09-949-016-33414	Sequence 13675, A
C	257	202	22.3	601	4	US-09-949-016-41049	Sequence 33414, A
C	258	202	22.3	168104	4	US-09-949-016-12026	Sequence 41049, A
C	259	202	22.3	168105	4	US-09-949-016-16554	Sequence 12026, A
C	260	201.8	22.2	27783	4	US-09-949-016-16736	Sequence 16554, A
C	261	201.8	22.2	5018	4	US-09-949-016-12315	Sequence 16736, A
C	262	201.8	22.2	51110	4	US-09-949-016-12059	Sequence 12315, A
C	263	201.8	22.2	51111	4	US-09-949-016-15724	Sequence 12069, A
C	264	201.8	22.2	56551	4	US-09-949-016-12030	Sequence 15724, A
C	265	201.8	22.2	58712	4	US-09-949-016-16651	Sequence 12030, A
C	266	201.8	22.2	60117	4	US-09-949-016-13312	Sequence 13312, A
C	267	201.8	22.2	60772	4	US-09-949-016-12707	Sequence 12702, A
C	268	201.8	22.2	6092	4	US-09-949-016-13741	Sequence 12702, A
C	269	201.8	22.2	84761	4	US-09-949-016-11919	Sequence 11919, A
C	270	201.8	22.2	84763	4	US-09-949-016-13914	Sequence 13914, A
C	271	201.8	22.2	13132	4	US-09-949-016-15535	Sequence 13914, A
C	272	201.8	22.2	177293	4	US-09-949-016-16513	Sequence 15535, A
C	273	201.8	22.2	234886	4	US-09-949-016-17272	Sequence 16513, A
C	274	201.8	22.2	28831	4	US-09-949-016-14854	Sequence 17272, A
C	275	201.8	22.2	4775	4	US-09-949-016-15683	Sequence 17272, A
C	276	201.6	22.2	84763	4	US-09-949-016-15683	Sequence 17272, A
C	277	201.6	22.2	29814	4	US-09-949-016-12390	Sequence 17272, A
C	278	201.6	22.2	46119	4	US-09-949-016-16981	Sequence 17272, A
C	279	201.6	22.2	46223	4	US-09-949-016-13267	Sequence 17272, A
C	280	201.6	22.2	50520	4	US-09-949-016-16659	Sequence 17272, A
C	281	201.6	22.2	246420	2	US-08-724-39A-20	Sequence 20, A
C	282	201.6	22.2	246240	2	US-08-724-39A-21	Sequence 21, A
C	283	201.6	22.2	246240	2	US-08-724-39A-22	Sequence 22, A
C	284	201.4	22.2	601	4	US-09-949-016-40426	Sequence 40426, A
C	285	201.4	22.2	601	4	US-09-949-016-16981	Sequence 169981, A
C	286	201.4	22.2	601	4	US-09-949-016-12526	Sequence 169981, A
C	287	201.4	22.2	601	4	US-09-949-016-13267	Sequence 169981, A
C	288	201.4	22.2	601	4	US-09-949-016-18171	Sequence 169981, A
C	289	201.4	22.2	601	4	US-09-949-016-18172	Sequence 169981, A
C	290	201.4	22.2	15739	4	US-09-949-016-11780	Sequence 169981, A
C	291	201.4	22.2	29655	4	US-09-949-016-12340	Sequence 169981, A
C	292	201.4	22.2	29771	4	US-09-949-016-12754	Sequence 169981, A
C	293	201.4	22.2	29771	4	US-09-949-016-13956	Sequence 169981, A
C	294	201.4	22.2	40655	4	US-09-949-016-12032	Sequence 169981, A
C	295	201.4	22.2	40655	4	US-09-949-016-15919	Sequence 169981, A
C	296	201.4	22.2	64467	4	US-09-949-016-12323	Sequence 169981, A
C	297	201.4	22.2	64467	4	US-10-949-016-4093	Sequence 3, A
C	298	201.4	22.2	68229	4	US-09-949-016-12140	Sequence 3, A
C	299	201.4	22.2	68229	4	US-09-949-016-15671	Sequence 3, A
C	300	201.2	22.2	32202	4	US-09-949-016-15357	Sequence 15671, A
C	301	201.2	22.2	68229	4	US-09-949-016-12140	Sequence 15671, A
C	302	201.2	22.2	68229	4	US-09-949-016-15671	Sequence 15671, A
C	303	201.2	22.2	79335	4	US-09-949-016-12456	Sequence 15671, A
C	304	201.2	22.2	79335	4	US-09-949-016-16121	Sequence 15671, A
C	305	201.2	22.2	16551	4	US-09-949-016-13032	Sequence 15671, A
C	306	201.2	22.2	256171	4	US-09-949-016-12822	Sequence 15671, A
C	307	201.2	22.2	256171	4	US-09-949-016-15524	Sequence 15671, A
C	308	201.2	22.2	601	4	US-09-949-016-12753	Sequence 15671, A
C	309	201.2	22.2	601	4	US-09-949-016-169369	Sequence 15671, A
C	310	201.2	22.2	601	4	US-09-949-016-16121	Sequence 15671, A
C	311	201.2	22.2	601	4	US-09-949-016-178914	Sequence 15671, A
C	312	201.2	22.2	8180	4	US-09-949-016-15370	Sequence 15671, A
C	313	201.2	22.2	9779	4	US-09-949-016-162753	Sequence 15671, A
C	314	201.2	22.2	14160	4	US-09-949-016-16894	Sequence 15671, A
C	315	201.2	22.2	34011	4	US-09-949-016-12485	Sequence 15671, A
C	316	201.2	22.2	44096	4	US-09-949-016-15208	Sequence 15671, A
C	317	201.2	22.2	81585	4	US-09-949-016-15427	Sequence 15671, A
C	318	201.2	22.2	98828	4	US-09-949-016-16630	Sequence 15671, A
C	319	201.2	22.2	108440	4	US-09-949-016-12065	Sequence 15671, A
C	320	201	22.2	108441	4	US-09-949-016-14090	Sequence 15671, A
C	321	201	22.2	16708	4	US-09-949-016-16423	Sequence 15671, A
C	322	201	22.2	4421	3	US-09-949-016-16423	Sequence 15671, A
C	323	200.8	22.1	4421	3	US-08-367-841A-9	Sequence 15671, A
C	324	200.8	22.1	4421	3	US-08-520-373D-6	Sequence 15671, A
C	325	200.8	22.1	4421	3	RCT-US95-07201-9	Sequence 15671, A
C	326	200.8	22.1	11729	4	US-09-949-016-13247	Sequence 15671, A
C	327	200.8	22.1	12797	4	US-09-949-016-13123	Sequence 15671, A
C	328	200.8	22.1	13455	4	US-09-949-016-13512	Sequence 15671, A
C	329	200.8	22.1	95122	4	US-09-949-016-17235	Sequence 15671, A
C	330	200.8	22.1	100928	4	US-09-949-016-6926	Sequence 15671, A
C	331	200.8	22.1	107820	4	US-09-949-016-156-1	Sequence 15671, A
C	332	200.8	22.1	319608	4	US-09-539-033D-1	Sequence 15671, A
C	333	200.8	22.1	319608	4	US-09-679-409-1	Sequence 15671, A
C	334	200.6	22.1	33987	4	US-09-949-016-12513	Sequence 15671, A
C	335	200.6	22.1	103987	4	US-09-949-016-16253	Sequence 15671, A
C	336	200.6	22.1	103988	4	US-09-949-016-17050	Sequence 15671, A
C	337	200.4	22.1	31867	4	US-09-949-016-17874	Sequence 15671, A
C	338	200.4	22.1	601	4	US-09-949-016-12166	Sequence 15671, A
C	339	200.4	22.1	601	4	US-09-949-016-15640	Sequence 15671, A
C	340	200.4	22.1	350	4	US-09-949-016-16268	Sequence 15671, A
C	341	200.4	22.1	350	4	US-09-949-016-12513	Sequence 15671, A
C	342	200.4	22.1	361	4	US-09-949-016-12151	Sequence 15671, A
C	343	200.4	22.1	361	4	US-09-949-016-16564	Sequence 15671, A
C	344	200.4	22.1	361	4	US-09-949-016-16708	Sequence 15671, A
C	345	200.4	22.1	361	4	US-09-949-016-16268	Sequence 15671, A
C	346	200.4	22.1	361	4	US-09-949-016-16508	Sequence 15671, A
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C	348	200.4	22.1	361	4	US-09-949-016-16874	Sequence 15671, A
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C	350	200.4	22.1	361	4	US-09-949-016-15764	Sequence 15671, A
C	351	200.4	22.1	361	4	US-09-949-016-16708	Sequence 15671, A
C	352	200.4	22.1	361	4	US-09-949-016-169919	Sequence 15671, A
C	353	200.4	22.1	361	4	US-09-949-016-18549	Sequence 15671, A
C	354	200.2	22.1	361	4	US-09-949-016-13136	Sequence 15671, A
C	355	200.2	22.1	361	4	US-09-949-016-13465	Sequence 15671, A
C	356	200.2	22.1	361	4	US-09-949-016-13076	Sequence 15671, A
C	357	200.2	22.1	361	4	US-09-949-016-12515	Sequence 15671, A
C	358	200.2	22.1	361	4	US-09-949-016-15338	Sequence 15671, A
C	359	200.2	22.1	361	4	US-09-949-016-169914	Sequence 15671, A
C	360	200.2	22.1	361	4	US-09-949-016-16538	Sequence 15671, A
C	361	200.2	22.1	361	4	US-09-949-016-17772	Sequence 15671, A
C	362	200.2	22.1	361	4	US-09-949-016-16251	Sequence 15671, A
C	363	200.2	22.1	361	4	US-09-949-016-15338	Sequence 15671, A
C	364	200.2	22.1	361	4	US-09-949-016-16538	Sequence 15671, A
C	365	200.2	22.1	361	4	US-09-949-016-16538	Sequence 15671, A
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C	369	200.2	22.1	361	4	US-09-949-016-16538	Sequence 15671, A
C	370	200.2	22.1	361	4	US-09-949-016-16538	Sequence 15671, A
C	371	200.2	22.1	361	4	US-09-949-016-	

C 393	200	22.1	64171	4	US-09-949-016-12502	Sequence 12502, A
C 394	200	22.1	73295	4	US-09-949-016-15151	Sequence 15151, A
C 395	200	22.1	14520	4	US-09-949-016-1858	Sequence 1558, A
C 396	200	22.1	19770	4	US-09-949-016-18220	Sequence 11820, A
C 397	200	22.1	192704	4	US-09-949-016-17182	Sequence 17182, A
C 398	200	22.1	203538	4	US-09-949-016-1505	Sequence 13505, A
C 399	200	22.1	678533	4	US-09-949-016-14577	Sequence 14577, A
C 400	200	22.1	678533	4	US-09-949-016-15778	Sequence 14578, A
C 401	199	22.0	601	4	US-09-949-016-36668	Sequence 39668, A
C 402	199	22.0	601	4	US-09-949-016-43315	Sequence 41315, A
C 403	199	22.0	601	4	US-09-949-016-43318	Sequence 43318, A
C 404	199	22.0	601	4	US-09-949-016-43319	Sequence 43319, A
C 405	199	22.0	601	4	US-09-949-016-43547	Sequence 43547, A
C 406	199	22.0	601	4	US-09-949-016-43548	Sequence 43548, A
C 407	199	22.0	601	4	US-09-949-016-43776	Sequence 43776, A
C 408	199	22.0	601	4	US-09-949-016-43777	Sequence 43777, A
C 409	199	22.0	601	4	US-09-949-016-43534	Sequence 47534, A
C 410	199	22.0	601	4	US-09-949-016-82428	Sequence 82428, A
C 411	199	22.0	601	4	US-09-949-016-187598	Sequence 187598, A
C 412	199	22.0	40546	4	US-09-949-016-1847	Sequence 12847, A
C 413	199	22.0	40546	4	US-09-949-016-1915	Sequence 12915, A
C 414	199	22.0	41578	4	US-09-949-016-15245	Sequence 15245, A
C 415	199	22.0	75480	4	US-09-949-016-15090	Sequence 16090, A
C 416	199	22.0	78720	4	US-09-949-016-17170	Sequence 16270, A
C 417	199	22.0	78720	4	US-09-949-016-17283	Sequence 17283, A
C 418	199	22.0	106924	4	US-09-949-016-18384	Sequence 13834, A
C 419	199	22.0	601	4	US-09-949-016-31382	Sequence 32182, A
C 420	199	22.0	601	4	US-09-949-016-60819	Sequence 60819, A
C 421	199	22.0	51062	4	US-09-949-016-1212131	Sequence 112131, A
C 422	199	22.0	601	4	US-09-949-016-146504	Sequence 146504, A
C 423	199	22.0	601	4	US-09-949-016-147535	Sequence 147535, A
C 424	199	22.0	263174	4	US-09-949-016-13839	Sequence 16389, A
C 425	199	22.0	32278	4	US-09-949-016-14575	Sequence 14578, A
C 426	199	22.0	36546	4	US-09-949-016-17543	Sequence 17543, A
C 427	199	22.0	51062	4	US-09-949-016-14725	Sequence 14725, A
C 428	199	22.0	10519	4	US-09-949-016-13029	Sequence 13029, A
C 429	199	22.0	601	4	US-09-949-016-61118	Sequence 64118, A
C 430	199	22.0	601	4	US-09-949-016-70685	Sequence 70685, A
C 431	199	22.0	601	4	US-09-949-016-70686	Sequence 70686, A
C 432	199	22.0	23826	4	US-09-949-016-16712	Sequence 16712, A
C 433	199	22.0	23826	4	US-09-949-016-16713	Sequence 16713, A
C 434	199	22.0	23826	4	US-09-949-016-16714	Sequence 16714, A
C 435	199	22.0	23826	4	US-09-949-016-16715	Sequence 16715, A
C 436	199	22.0	43192	4	US-09-949-016-16746	Sequence 15466, A
C 437	199	22.0	93971	4	US-09-949-016-16997	Sequence 16097, A
C 438	199	22.0	93971	4	US-09-949-016-16998	Sequence 16098, A
C 439	199	22.0	145928	4	US-09-949-016-13444	Sequence 15444, A
C 440	199	22.0	17606	4	US-09-949-016-16804	Sequence 16804, A
C 441	199	22.0	253375	4	US-09-949-016-12849	Sequence 12849, A
C 442	199	22.0	601	4	US-09-949-016-65950	Sequence 69950, A
C 443	199	22.0	601	4	US-09-949-016-76001	Sequence 76001, A
C 444	199	22.0	29913	4	US-09-949-016-12481	Sequence 13395, A
C 445	199	22.0	31822	4	US-09-949-016-13356	Sequence 12481, A
C 446	199	22.0	37225	4	US-09-949-016-15526	Sequence 13356, A
C 447	199	22.0	91279	4	US-09-949-016-15146	Sequence 15145, A
C 448	199	22.0	100463	4	US-09-949-016-15151	Sequence 12511, A
C 449	199	22.0	100463	4	US-09-949-016-15152	Sequence 12512, A
C 450	199	22.0	194537	4	US-09-949-016-15294	Sequence 13725, A
C 451	199	22.0	201529	4	US-09-949-016-12740	Sequence 12928, A
C 452	199	22.0	304533	4	US-09-949-016-15371	Sequence 15226, A
C 453	199	22.0	304533	4	US-09-949-016-15372	Sequence 15372, A
C 454	199	22.1	601	4	US-09-949-016-68387	Sequence 18137, A
C 455	199	22.1	8374	4	US-09-949-016-12575	Sequence 15257, A
C 456	199	22.1	10546	4	US-09-949-016-16264	Sequence 15624, A
C 457	199	22.1	17154	4	US-09-949-016-16889	Sequence 16889, A
C 458	199	22.1	19503	4	US-09-949-016-16528	Sequence 16528, A
C 459	199	22.1	24205	4	US-09-949-016-15385	Sequence 15385, A
C 460	199	22.1	39982	4	US-09-949-016-1243	Sequence 18137, A
C 461	199	22.1	39982	4	US-09-949-016-1257	Sequence 15257, A
C 462	199	22.1	40493	4	US-09-949-016-15453	Sequence 15453, A
C 463	199	22.1	51043	4	US-09-949-016-12739	Sequence 12739, A
C 464	199	22.1	51043	4	US-09-949-016-12739	Sequence 12739, A
C 465	199	22.1	51043	4	US-09-949-016-13946	Sequence 13946, A
C 466	199	22.1	64171	4	US-09-949-016-12286	Sequence 12286, A
C 467	199	22.1	73295	4	US-09-949-016-15132	Sequence 15132, A
C 468	199	22.1	14520	4	US-09-949-016-13517	Sequence 13517, A
C 469	199	22.1	19770	4	US-09-949-016-13518	Sequence 13518, A
C 470	199	22.1	192704	4	US-09-949-016-13694	Sequence 13694, A
C 471	199	22.1	203538	4	US-09-949-016-15095	Sequence 15095, A
C 472	199	22.1	678533	4	US-09-949-016-14913	Sequence 14913, A
C 473	199	22.1	678533	4	US-09-949-016-14914	Sequence 14914, A
C 474	199	22.1	678533	4	US-09-949-016-14915	Sequence 14915, A
C 475	199	22.1	678533	4	US-09-949-016-14916	Sequence 14916, A
C 476	199	22.1	678533	4	US-09-949-016-14917	Sequence 14917, A
C 477	199	22.1	678533	4	US-09-949-016-14918	Sequence 14918, A
C 478	199	22.1	678533	4	US-09-949-016-14919	Sequence 14919, A
C 479	199	22.1	678533	4	US-09-949-016-14920	Sequence 14920, A
C 480	199	22.1	678533	4	US-09-949-016-14921	Sequence 14921, A
C 481	199	22.1	678533	4	US-09-949-016-14922	Sequence 14922, A
C 482	199	22.1	678533	4	US-09-949-016-14923	Sequence 14923, A
C 483	199	22.1	678533	4	US-09-949-016-14924	Sequence 14924, A
C 484	199	22.1	678533	4	US-09-949-016-14925	Sequence 14925, A
C 485	199	22.1	678533	4	US-09-949-016-14926	Sequence 14926, A
C 486	199	22.1	678533	4	US-09-949-016-14927	Sequence 14927, A
C 487	199	22.1	678533	4	US-09-949-016-14928	Sequence 14928, A
C 488	199	22.1	678533	4	US-09-949-016-14929	Sequence 14929, A
C 489	199	22.1	678533	4	US-09-949-016-14930	Sequence 14930, A
C 490	199	22.1	678533	4	US-09-949-016-14931	Sequence 14931, A
C 491	199	22.1	678533	4	US-09-949-016-14932	Sequence 14932, A
C 492	199	22.1	678533	4	US-09-949-016-14933	Sequence 14933, A
C 493	199	22.1	678533	4	US-09-949-016-14934	Sequence 14934, A
C 494	199	22.1	678533	4	US-09-949-016-14935	Sequence 14935, A
C 495	199	22.1	678533	4	US-09-949-016-14936	Sequence 14936, A
C 496	199	22.1	678533	4	US-09-949-016-14937	Sequence 14937, A
C 497	199	22.1	678533	4	US-09-949-016-14938	Sequence 14938, A
C 498	199	22.1	678533	4	US-09-949-016-14939	Sequence 14939, A
C 499	199	22.1	678533	4	US-09-949-016-14940	Sequence 14940, A
C 500	199	22.1	678533	4	US-09-949-016-14941	Sequence 14941, A
C 501	199	22.1	678533	4	US-09-949-016-14942	Sequence 14942, A
C 502	199	22.1	678533	4	US-09-949-016-14943	Sequence 14943, A
C 503	199	22.1	678533	4	US-09-949-016-14944	Sequence 14944, A
C 504	199	22.1	678533	4	US-09-949-016-14945	Sequence 14945, A
C 505	199	22.1	678533	4	US-09-949-016-14946	Sequence 14946, A
C 506	199	22.1	678533	4	US-09-949-016-14947	Sequence 14947, A
C 507	199	22.1	678533	4	US-09-949-016-14948	Sequence 14948, A
C 508	199	22.1	678533	4	US-09-949-016-14949	Sequence 14949, A
C 509	199	22.1	678533	4	US-09-949-016-14950	Sequence 14950, A
C 510	199	22.1	678533	4	US-09-949-016-14951	Sequence 14951, A
C 511	199	22.1	678533	4	US-09-949-016-14952	Sequence 14952, A
C 512	199	22.1	678533	4	US-09-949-016-14953	Sequence 14953, A
C 513	199	22.1	678533	4	US-09-949-016-14954	Sequence 14954, A
C 514	199	22.1	678533	4	US-09-949-016-14955	Sequence 14955, A
C 515	199	22.1	678533	4	US-09-949-016-14956	Sequence 14956, A
C 516	199	22.1	678533	4	US-09-949-016-14957	Sequence 14957, A
C 517	199	22.1	678533	4	US-09-949-016-14958	Sequence 14958, A
C 518	199	22.1	678533	4	US-09-949-016-14959	Sequence 14959, A
C 519	199	22.1	678533	4	US-09-949-016-14960	Sequence 14960, A
C 520	199	22.1	678533	4	US-09-949-016-14961	Sequence 14961, A
C 521	199	22.1	678533	4	US-09-949-016-14962	Sequence 14962, A
C 522	199	22.1	678533	4	US-09-949-016-14963	Sequence 14963, A
C 523	199	22.1	678533	4	US-09-949-016-14964	Sequence 14964, A
C 524	199	22.1	678533	4	US-09-949-016-1	

C	539	198.4	21.9	601	4	US-09-949-016-150106	Sequence 150106,	c	612	198	21.8	601	4	US-09-949-016-44634
C	540	198.4	21.9	601	4	US-09-949-016-15639	Sequence 15639,	c	613	198	21.8	601	4	US-09-949-016-89078
C	541	198.4	21.9	601	4	US-09-949-016-171105	Sequence 171105,	c	614	198	21.8	601	4	US-09-949-016-136816
C	542	198.4	21.9	601	4	US-09-949-016-171105	Sequence 171235,	c	615	198	21.8	601	4	US-09-949-016-140334
C	543	198.4	21.9	7705	2	US-08-607-080-115	Sequence 115, APP	c	615	198	21.8	601	4	US-09-949-016-10107
C	544	198.4	21.9	1586	4	US-09-949-016-13899	Sequence 13899,	c	617	198	21.8	601	4	US-09-949-016-160816
C	545	198.4	21.9	20441	4	US-09-949-016-13052	Sequence 13052,	c	618	198	21.8	601	4	US-09-949-016-164502
C	546	198.4	21.9	22010	4	US-09-949-016-15960	Sequence 15960,	c	619	198	21.8	601	4	US-09-949-016-172475
C	547	198.4	21.9	40333	4	US-09-949-016-11821	Sequence 11821,	c	620	198	21.8	601	4	US-09-949-016-16376
C	548	198.4	21.9	40342	4	US-09-949-016-13982	Sequence 13982,	c	621	198	21.8	601	4	US-09-949-016-16773
C	549	198.4	21.9	45227	4	US-09-949-016-16243	Sequence 16243,	c	622	198	21.8	601	4	US-09-949-016-19473
C	550	198.4	21.9	50797	4	US-09-949-016-16345	Sequence 16346,	c	623	198	21.8	601	4	US-09-949-016-16347
C	551	198.4	21.9	50797	4	US-09-949-016-16347	Sequence 16347,	c	624	198	21.8	601	4	US-09-949-016-17474
C	552	198.4	21.9	51773	4	US-09-949-016-13018	Sequence 13018,	c	625	198	21.8	601	4	US-09-949-016-164502
C	553	198.4	21.9	72778	4	US-09-949-016-16113	Sequence 16113,	c	626	198	21.8	601	4	US-09-949-016-17470
C	554	198.4	21.9	85054	4	US-09-949-016-12908	Sequence 12908,	c	627	198	21.8	601	4	US-09-949-016-13471
C	555	198.4	21.9	10729	4	US-09-949-016-12663	Sequence 12663,	c	628	198	21.8	601	4	US-09-949-016-16773
C	556	198.4	21.9	107329	4	US-09-949-016-12664	Sequence 12664,	c	629	198	21.8	601	4	US-09-949-016-15475
C	557	198.4	21.9	107351	4	US-09-949-016-15408	Sequence 15408,	c	630	198	21.8	601	4	US-09-949-016-172475
C	558	198.4	21.9	107330	4	US-09-949-016-15409	Sequence 15409,	c	631	198	21.8	601	4	US-09-949-016-17470
C	559	198.4	21.9	107330	4	US-09-949-016-15410	Sequence 15410,	c	632	198	21.8	601	4	US-09-949-016-17471
C	560	198.4	21.9	107330	4	US-09-949-016-15411	Sequence 15411,	c	633	198	21.8	601	4	US-09-949-016-17472
C	561	198.4	21.9	107350	4	US-09-949-016-12662	Sequence 12662,	c	634	198	21.8	601	4	US-09-949-016-19473
C	562	198.4	21.9	10751	4	US-09-949-016-15412	Sequence 15412,	c	635	198	21.8	601	4	US-09-949-016-16193
C	563	198.4	21.9	10751	4	US-09-949-016-15413	Sequence 15413,	c	636	198	21.8	601	4	US-09-949-016-17454
C	564	198.4	21.9	10751	4	US-09-949-016-15414	Sequence 15414,	c	637	198	21.8	601	4	US-09-949-016-16151
C	565	198.4	21.9	10751	4	US-09-949-016-15415	Sequence 15415,	c	638	198	21.8	601	4	US-09-949-016-16054
C	566	198.4	21.9	10725	4	US-09-949-016-15415	Sequence 15415,	c	639	198	21.8	601	4	US-09-949-016-16792
C	567	198.4	21.9	10796	4	US-09-949-016-15404	Sequence 15404,	c	640	198	21.8	601	4	US-09-949-016-109524
C	568	198.4	21.9	10726	4	US-09-949-016-15405	Sequence 15405,	c	641	197.8	21.8	601	4	US-09-949-016-109777
C	569	198.4	21.9	10726	4	US-09-949-016-15405	Sequence 15405,	c	642	197.8	21.8	601	4	US-09-949-016-13748
C	570	198.4	21.9	10796	4	US-09-949-016-15407	Sequence 15407,	c	643	197.8	21.8	601	4	US-09-949-016-148576
C	571	198.4	21.9	13358	4	US-09-949-016-16964	Sequence 16964,	c	644	197.8	21.8	601	4	US-09-949-016-148592
C	572	198.4	21.9	13360	4	US-09-949-016-169651	Sequence 169651,	c	645	197.8	21.8	601	4	US-09-949-016-164117
C	573	198.4	21.9	149971	4	US-09-949-016-13590	Sequence 13590,	c	646	197.8	21.8	601	4	US-09-949-016-104524
C	574	198.4	21.9	19133	4	US-09-949-016-16144	Sequence 16144,	c	647	197.8	21.8	601	4	US-09-949-016-150708
C	575	198.4	21.9	268449	4	US-09-949-016-17244	Sequence 17244,	c	648	197.8	21.8	601	4	US-09-949-016-16198
C	576	198.4	21.9	21056	4	US-09-949-016-17302	Sequence 17302,	c	649	197.8	21.8	601	4	US-09-949-016-17538
C	577	198.4	21.9	21056	4	US-09-949-016-173303	Sequence 173303,	c	650	197.8	21.8	601	4	US-09-949-016-17310
C	578	198.4	21.9	21056	4	US-09-949-016-17693	Sequence 17693,	c	651	197.8	21.8	601	4	US-09-949-016-18583
C	579	198.4	21.9	21056	4	US-09-949-016-186050	Sequence 186050,	c	652	197.8	21.8	601	4	US-09-949-016-150707
C	580	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	653	197.8	21.8	601	4	US-09-949-016-13151
C	581	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	654	197.8	21.8	601	4	US-09-949-016-16198
C	582	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	655	197.8	21.8	601	4	US-09-949-016-17538
C	583	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	656	197.8	21.8	601	4	US-09-949-016-17538
C	584	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	657	197.8	21.8	601	4	US-09-949-016-17577
C	585	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	658	197.8	21.8	601	4	US-09-949-016-150707
C	586	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	659	197.8	21.8	601	4	US-09-949-016-150708
C	587	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	660	197.8	21.8	601	4	US-09-949-016-150708
C	588	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	661	197.8	21.8	601	4	US-09-949-016-150708
C	589	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	662	197.8	21.8	601	4	US-09-949-016-150708
C	590	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	663	197.8	21.8	601	4	US-09-949-016-150708
C	591	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	664	197.8	21.8	601	4	US-09-949-016-150708
C	592	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	665	197.8	21.8	601	4	US-09-949-016-150708
C	593	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	666	197.8	21.8	601	4	US-09-949-016-150708
C	594	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	667	197.8	21.8	601	4	US-09-949-016-150708
C	595	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	668	197.8	21.8	601	4	US-09-949-016-150708
C	596	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	669	197.8	21.8	601	4	US-09-949-016-150708
C	597	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	670	197.8	21.8	601	4	US-09-949-016-150708
C	598	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	671	197.8	21.8	601	4	US-09-949-016-150708
C	599	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	672	197.8	21.8	601	4	US-09-949-016-150708
C	600	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	673	197.8	21.8	601	4	US-09-949-016-150708
C	601	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	674	197.8	21.8	601	4	US-09-949-016-150708
C	602	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	675	197.8	21.8	601	4	US-09-949-016-150708
C	603	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	676	197.8	21.8	601	4	US-09-949-016-150708
C	604	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	677	197.8	21.8	601	4	US-09-949-016-150708
C	605	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	678	197.8	21.8	601	4	US-09-949-016-150708
C	606	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	679	197.8	21.8	601	4	US-09-949-016-150708
C	607	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	680	197.8	21.8	601	4	US-09-949-016-150708
C	608	198.4	21.9	21056	4	US-09-949-016-18247	Sequence 18247,	c	681	197.8	21.8	601	4	

C	685	197.6	21.8	601	4	US-09-949-016-116409	Sequence 116409,	758	197.2	41125	4	US-09-949-016-12413	Sequence 12413, A			
C	686	197.6	21.8	601	4	US-09-949-016-116518	Sequence 116518,	759	197.2	21.7	41126	4	US-09-949-016-12723	Sequence 1723, A		
C	687	197.6	21.8	601	4	US-09-949-016-116484	Sequence 116484,	760	197.2	21.7	61461	4	US-09-949-016-16484	Sequence 16484, A		
C	688	197.6	21.8	38808	4	US-09-949-016-11802	Sequence 11802,	761	197.2	21.7	62908	4	US-09-949-016-17554	Sequence 17554, A		
C	689	197.6	21.8	38808	4	US-09-949-016-116735	Sequence 116735,	762	197.2	21.7	67610	4	US-09-949-016-15521	Sequence 15521, A		
C	690	197.6	21.8	46343	4	US-09-949-016-116242	Sequence 11624,	763	197.2	21.7	83697	4	US-09-949-016-116040	Sequence 16040, A		
C	691	197.6	21.8	51508	4	US-09-949-016-16881	Sequence 11681,	764	197.2	21.7	85854	4	US-09-949-016-12908	Sequence 12908, A		
C	692	197.6	21.8	59319	4	US-09-949-016-16115	Sequence 116115,	759	197.2	21.7	92139	4	US-09-949-016-17273	Sequence 17273, A		
C	693	197.6	21.8	66164	4	US-09-949-016-15754	Sequence 115754,	760	197.2	21.7	61461	4	US-09-949-016-16484	Sequence 16484, A		
C	694	197.6	21.8	19762	4	US-09-949-016-157313	Sequence 115731,	761	197.2	21.7	62908	4	US-09-949-016-17554	Sequence 17554, A		
C	695	197.6	21.8	11981	4	US-09-949-016-11846	Sequence 11844,	762	197.2	21.7	76610	4	US-09-949-016-15521	Sequence 15521, A		
C	701	197.4	21.8	601	4	US-09-949-016-21510	Sequence 11510,	763	197.2	21.7	83697	4	US-09-949-016-116040	Sequence 16040, A		
C	702	197.4	21.8	19982	4	US-09-949-016-36770	Sequence 113606,	764	197.2	21.7	601	4	US-09-949-016-113846	Sequence 113846, A		
C	703	197.4	21.8	139150	4	US-09-949-016-17398	Sequence 117398,	765	197.2	21.7	92139	4	US-09-949-016-114014	Sequence 114014, A		
C	698	197.6	21.8	139577	4	US-09-949-016-12879	Sequence 112879,	766	197.2	21.7	92139	4	US-09-949-016-114182	Sequence 114182, A		
C	704	197.4	21.8	199915	4	US-09-949-016-15884	Sequence 115884,	771	197.2	21.7	601	4	US-09-949-016-114350	Sequence 114350, A		
C	705	197.4	21.8	300402	4	US-09-949-016-13432	Sequence 113432,	772	197.2	21.7	248968	4	US-09-949-016-12614	Sequence 12614, A		
C	706	197.5	21.8	4	US-09-949-016-123143	Sequence 1123143,	773	197.2	21.7	601	4	US-09-949-016-114513	Sequence 114513, A			
C	707	197.4	21.8	601	4	US-09-949-016-123143	Sequence 1123143,	774	197.2	21.7	601	4	US-09-949-016-114854	Sequence 114854, A		
C	708	197.4	21.8	601	4	US-09-949-016-123237	Sequence 1123237,	775	197.2	21.7	601	4	US-09-949-016-114014	Sequence 114014, A		
C	709	197.4	21.8	601	4	US-09-949-016-123331	Sequence 112331,	776	197.2	21.7	601	4	US-09-949-016-115022	Sequence 115022, A		
C	710	197.4	21.8	601	4	US-09-949-016-123373	Sequence 1123373,	777	197.2	21.7	8396	3	US-09-949-016-174A-1	Sequence 174A-1, A		
C	711	197.4	21.8	601	4	US-09-949-016-122955	Sequence 1122955,	778	197.2	21.7	8409	3	US-09-949-016-117817	Sequence 117817, A		
C	712	197.4	21.8	601	4	US-09-949-016-123454	Sequence 1123454,	779	197.2	21.7	15615	4	US-09-949-016-17221	Sequence 117221, A		
C	713	197.4	21.8	601	4	US-09-949-016-123499	Sequence 1123499,	780	197.2	21.7	18319	4	US-09-949-016-17446	Sequence 117446, A		
C	714	197.4	21.8	601	4	US-09-949-016-123541	Sequence 1123541,	781	197.2	21.7	20610	4	US-09-949-016-14610	Sequence 14610, A		
C	715	197.4	21.8	601	4	US-09-949-016-123583	Sequence 1123583,	782	197.2	21.7	32327	4	US-09-949-016-114018	Sequence 114018, A		
C	716	197.4	21.8	601	4	US-09-949-016-123625	Sequence 1123625,	783	197.2	21.7	45454	4	US-09-949-016-12681	Sequence 12681, A		
C	717	197.4	21.8	601	4	US-09-949-016-123667	Sequence 1123667,	784	197.2	21.7	34548	4	US-09-949-016-167681	Sequence 167681, A		
C	718	197.4	21.8	601	4	US-09-949-016-123709	Sequence 1123709,	785	197.2	21.7	39032	4	US-09-949-016-12874	Sequence 12874, A		
C	719	197.4	21.8	601	4	US-09-949-016-123751	Sequence 1123751,	786	197.2	21.7	39039	4	US-09-949-016-16462	Sequence 16462, A		
C	720	197.4	21.8	601	4	US-09-949-016-128053	Sequence 1128053,	787	197.2	21.7	416348	4	US-09-949-016-15471	Sequence 15471, A		
C	721	197.4	21.8	601	4	US-09-949-016-12829	Sequence 112829,	788	197.2	21.7	44608	4	US-09-949-016-15604	Sequence 15604, A		
C	722	197.4	21.8	601	4	US-09-949-016-171104	Sequence 117104,	789	197.2	21.7	4971	21.7	47480	4	US-09-949-016-17049	Sequence 17049, A
C	723	197.4	21.8	601	4	US-09-949-016-171234	Sequence 1171234,	790	197.2	21.7	56665	4	US-09-949-016-14026	Sequence 14026, A		
C	724	197.4	21.8	601	4	US-09-949-016-178113	Sequence 1178113,	791	197.2	21.7	60424	4	US-09-949-016-12175	Sequence 12175, A		
C	725	197.4	21.8	15148	4	US-09-949-016-15058	Sequence 115058,	792	197.2	21.7	65300	4	US-09-949-016-15813	Sequence 15813, A		
C	726	197.4	21.8	27555	4	US-09-949-016-17466	Sequence 117466,	793	197.2	21.7	66428	4	US-09-949-016-12917	Sequence 12917, A		
C	727	197.4	21.8	31469	4	US-09-949-016-17335	Sequence 117335,	794	197.2	21.7	77535	4	US-09-949-016-14279	Sequence 14279, A		
C	728	197.4	21.8	34230	4	US-09-949-016-12052	Sequence 112052,	795	197.2	21.7	77535	4	US-09-949-016-14281	Sequence 14281, A		
C	729	197.4	21.8	38954	4	US-09-949-016-12892	Sequence 112892,	796	197.2	21.7	77535	4	US-09-949-016-14026	Sequence 14026, A		
C	730	197.4	21.8	79350	4	US-09-949-016-124675	Sequence 1124675,	797	197.2	21.7	107421	4	US-09-949-016-15532	Sequence 15532, A		
C	731	197.4	21.8	79351	4	US-09-949-016-162675	Sequence 1162675,	798	197.2	21.7	11709	4	US-09-949-016-12085	Sequence 12085, A		
C	732	197.4	21.8	84875	4	US-09-949-016-17334	Sequence 117334,	799	197.2	21.7	121982	4	US-09-949-016-129105	Sequence 129105, A		
C	733	197.4	21.8	84875	4	US-09-949-016-17335	Sequence 117335,	800	197.2	21.7	133719	4	US-09-949-016-15092	Sequence 15092, A		
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C	736	197.4	21.8	85152	4	US-09-949-016-12665	Sequence 112665,	803	197.2	21.7	601	4	US-09-949-016-109491	Sequence 109491, A		
C	737	197.4	21.8	85152	4	US-09-949-016-12666	Sequence 112666,	804	197.2	21.7	601	4	US-09-949-016-162049	Sequence 162049, A		
C	738	197.4	21.8	85152	4	US-09-949-016-12667	Sequence 112667,	805	197.2	21.7	601	4	US-09-949-016-165965	Sequence 165965, A		
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C	744	197.4	21.8	85152	4	US-09-949-016-12668	Sequence 112668,	811	197.2	21.7	35417	4	US-09-949-016-16129	Sequence 16129, A		
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992	196.2	21.6	121970	4	US-09-949-016-17206	Sequence 17206, A	c1065	195.8	21.6	601	4	Sequence 123624,
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c1159	195.4	21.5	23172	4	US-09-949-016-16307	Sequence 16193, A	c1232	195.2	21.5	48108	4	US-09-949-016-1382
c1160	195.4	21.5	53332	4	US-10-224-562-3	Sequence 13074, A	c1233	195.2	21.5	48108	4	US-09-949-016-1382
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c1162	195.4	21.5	57054	4	US-09-949-016-14159	Sequence 17080, A	c1235	195.2	21.5	48108	4	US-09-949-016-1382
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c1164	195.4	21.5	67586	4	US-09-949-016-16519	Sequence 15675, A	c1237	195.2	21.5	48108	4	US-09-949-016-1382
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c1168	195.4	21.5	92276	4	US-09-949-016-12166	Sequence 14159, A	c1241	195.2	21.5	48108	4	US-09-949-016-1382
c1169	195.4	21.5	102009	4	US-09-949-016-16617	Sequence 13983, A	c1242	195.2	21.5	48108	4	US-09-949-016-1382
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c1177	195.4	21.5	518128	4	US-09-949-016-14545	Sequence 16617, A	c1250	195.2	21.5	48108	4	US-09-949-016-1382
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c1195												

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c1271	195	21.5	61140	4	US-09-949-016-15771	Sequence 15771, A
c1272	195	21.5	66219	4	US-09-949-016-12038	Sequence 12038, A
c1273	195	21.5	66219	4	US-09-949-016-12038	Sequence 12038, A
c1274	195	21.5	66227	4	US-09-949-016-15303	Sequence 15303, A
c1275	195	21.5	66227	4	US-09-949-016-15303	Sequence 15303, A
c1276	195	21.5	75395	4	US-09-984-890-3	Sequence 3, Appli
c1277	195	21.5	75395	4	US-10-274-194-3	Sequence 3, Appli
c1278	195	21.5	82000	4	US-09-949-016-15595	Sequence 15595, A
c1279	195	21.5	84587	4	US-09-949-016-15733	Sequence 15733, A
c1280	195	21.5	86213	4	US-09-949-016-17240	Sequence 17240, A
c1281	195	21.5	86213	4	US-09-949-016-17241	Sequence 17241, A
c1282	195	21.5	86213	4	US-09-949-016-17242	Sequence 17242, A
c1283	195	21.5	86213	4	US-09-949-016-17243	Sequence 17243, A
c1284	195	21.5	100877	4	US-09-949-016-17276	Sequence 13276, A
c1285	195	21.5	119801	4	US-09-949-016-13453	Sequence 13453, A
c1286	195	21.5	123863	4	US-09-949-016-14202	Sequence 14202, A
c1287	194.8	21.5	601	4	US-09-949-016-17302	Sequence 70398, A
c1288	194.8	21.5	601	4	US-09-949-016-17309	Sequence 70399, A
c1289	194.8	21.5	601	4	US-09-949-016-121140	Sequence 121140, A
c1290	194.8	21.5	601	4	US-09-949-016-124427	Sequence 124427, A
c1291	194.8	21.5	601	4	US-09-949-016-180851	Sequence 180851, A
c1292	194.8	21.5	601	4	US-09-949-016-183999	Sequence 183999, A
c1293	194.8	21.5	601	4	US-09-949-016-184104	Sequence 184104, A
c1294	194.8	21.5	601	4	US-09-949-016-184209	Sequence 184209, A
c1295	194.8	21.5	601	4	US-09-949-016-184314	Sequence 184314, A
c1296	194.8	21.5	601	4	US-09-949-016-189485	Sequence 189485, A
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c1298	194.8	21.5	25769	4	US-09-949-016-17154	Sequence 17154, A
c1299	194.8	21.5	29453	4	US-09-949-016-12939	Sequence 12939, A
c1300	194.8	21.5	29453	4	US-09-949-016-184240	Sequence 184240, A
c1301	194.8	21.5	29453	4	US-09-949-016-12941	Sequence 12941, A
c1302	194.8	21.5	29453	4	US-09-949-016-189482	Sequence 189482, A
c1303	194.8	21.5	31602	4	US-09-949-016-16961	Sequence 16961, A
c1304	194.8	21.5	36759	4	US-09-949-016-12216	Sequence 12216, A
c1305	194.8	21.5	36760	4	US-09-949-016-14021	Sequence 14021, A
c1306	194.8	21.5	38346	4	US-09-949-016-14502	Sequence 14502, A
c1307	194.8	21.5	39754	4	US-09-949-016-14689	Sequence 14689, A
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c1313	194.8	21.5	48682	4	US-09-949-016-17239	Sequence 17239, A
c1314	194.8	21.5	48682	4	US-09-949-016-17135	Sequence 17135, A
c1315	194.8	21.5	51022	4	US-09-949-016-17136	Sequence 17136, A
c1316	194.8	21.5	51022	4	US-09-949-016-17137	Sequence 17137, A
c1317	194.8	21.5	51022	4	US-09-949-016-17138	Sequence 17138, A
c1318	194.8	21.5	69752	4	US-09-949-016-14094	Sequence 14094, A
c1319	194.8	21.5	75216	4	US-09-949-016-14061	Sequence 14061, A
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c1322	194.8	21.5	86213	4	US-09-949-016-17240	Sequence 17240, A
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c1325	194.8	21.5	86213	4	US-09-949-016-17243	Sequence 17243, A
c1326	194.8	21.5	86380	4	US-09-949-016-14837	Sequence 14837, A
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c1330	194.8	21.5	11212	4	US-09-949-016-15639	Sequence 15639, A
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c1336	194.8	21.5	250352	4	US-09-949-016-16742	Sequence 16742, A
c1337	194.8	21.5	39084	4	US-09-949-016-17420	Sequence 17420, A
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c1340	194.8	21.5	601	4	US-09-949-016-18127	Sequence 18127, A
c1341	194.6	21.5	601	4	US-09-949-016-154652	Sequence 154652, A

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C1417	194.4	21.4	54246	4	US-09-949-016-16206	Sequence 16206, A	C1490	194.2	21.4	151088	4	US-09-949-016-16240	Sequence 16240, A
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C1425	194.4	21.4	84162	4	US-09-949-016-12670	Sequence 12570, A	C1498	194.2	21.4	251682	4	US-09-949-016-11973	Sequence 17631, A
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C1429	194.4	21.4	87869	4	US-09-949-016-15045	Sequence 15045, A							
C1430	194.4	21.4	87869	4	US-09-949-016-15046	Sequence 15046, A							
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C1442	194.2	21.4	601	4	US-09-949-016-96520	Sequence 96520, A							
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C1445	194.2	21.4	601	4	US-09-949-016-97318	Sequence 97318, A							
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C1464	194.2	21.4	601	4	US-09-949-016-10238	Sequence 102388, A							
C1465	194.2	21.4	601	4	US-09-949-016-102438	Sequence 102438, A							
C1466	194.2	21.4	601	4	US-09-949-016-132686	Sequence 132686, A							
C1467	194.2	21.4	601	4	US-09-949-016-139110	Sequence 139110, A							
C1468	194.2	21.4	601	4	US-09-949-016-143344	Sequence 143344, A							
C1469	194.2	21.4	601	4	US-09-949-016-143515	Sequence 143515, A							
C1470	194.2	21.4	601	4	US-09-949-016-154653	Sequence 154653, A							
C1471	194.2	21.4	601	4	US-09-949-016-186006	Sequence 186006, A							
C1472	194.2	21.4	601	4	US-09-949-016-186116	Sequence 186116, A							
C1473	194.2	21.4	601	4	US-09-949-016-186186	Sequence 186186, A							
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C1475	194.2	21.4	14961	4	US-09-949-016-13400	Sequence 13400, A							
C1476	194.2	21.4	15084	4	US-09-949-016-16277	Sequence 16277, A							
C1477	194.2	21.4	20674	4	US-09-949-016-186006	Sequence 186006, A							
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C1483	194.2	21.4	43675	4	US-09-949-016-13777	Sequence 13777, A							
C1484	194.2	21.4	57857	4	US-09-949-016-13152	Sequence 13152, A							
C1485	194.2	21.4	63187	4	US-09-949-016-12682	Sequence 12682, A							
C1486	194.2	21.4	63187	4	US-09-949-016-16288	Sequence 16288, A							
C1487	194.2	21.4	84425	4	US-09-949-016-17402	Sequence 17402, A							

Patent No. 6012339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT FILING NUMBER: US/09/949, 016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241, 755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237, 768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231, 498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12969

LENGTH: 36148

TYPE: DNA

ORGANISM: Human

US-09-949-016-12969

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RESULT 10
 US-09-949-016-12682
 ; Sequence 12682, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241, 755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237, 768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231, 498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 16288
 ; LENGTH: 63187
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-16288
 Query Match 23.2%; Score 210.4; DB 4; Length 63187;
 Best Local Similarity 82.9%; Pred. No. 2.3e-54; Mismatches 0; Indels 1; Gaps 1;
 Matches 252; Conservative 0; Mismatches 51; Indels 1; Gaps 1;
 Qy 605 ATTAAGTCTGAAATGGCCGGACGGCTCAAGCTTAATCCACACTTG 664
 Db 8887 ATTAACTTAATGCTGTGGCGGGACGGCTCAAGCTTAATCCACACTTG 8946
 Qy 665 AGGCCGAGCGCGTGAACCTGAGATCAGGAGTCAGAACCCCTGGCAATG 724
 Db 8947 AGGTGAGGGGTGATCACTTGGTAGGTAGGAGTCAGAACCCCTGGCAATG 9006
 Qy 725 GAAACCTTGCTACTAAATACTAAAATAGCCAGGAGCAGTGTGTOCACTGT 784
 Db 9007 GAAACCCGCTACTAAATACTAAAATAGTGGATGGCTGGCAAGGCTGGCAATG 9066
 Qy 785 CCCAGTTACTGGGAGCTGGCTGAGTCAGGAGTCAGAACCCGTGAGCCAGGT 844
 Db 9007 GAAACCCGCTACTAAATACTAAAATAGTGGATGGCTGAGTCAGAACCCGTGAGT 9066
 Qy 845 GTGAGCGAGATGGCGCGCTG-ATTCCGCCTGGCGAAGAGTGAACTCCATCTCA 903
 Db 9127 GTGAGCGAGATGGCGCTGCACTGCAATCCACCTGGAGCAAGAGTGAACTCTCTCA 9186
 Qy 904 CACA 907
 Db 9187 AAAA 9190
 RESULT 12
 US-09-949-016-12786/c
 ; Sequence 12786, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241, 755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237, 768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231, 498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 12786
 ; LENGTH: 35678
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-12786
 RESULT 11
 US-09-949-016-16288
 ; Sequence 16288, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.

Query Match 23.1%; Score 209.2; DB 4; Length 35678;
 Best Local Similarity 79.7%; Pred. No. 4e-54; Mismatches 63; Indels 0; Gaps 0;
 Matches 247; Conservative 0; N mismatches 0;

QY 598 ATTAGCAATTAAACTGAGAATGGCGGGACGGTGTGCTAACGCCCTGTAATCCAGCA 657
 Db 10261 ATATGTTAAATAATAGAGAGCAGGAGCTGGCACAGTGCTATGCTTATATCCAGCA 10202
 Db 10201 CTTTGGGAGGCCGAGGGGGTGTGATCAGCTGAGATCAGGAGTCAGCCAGCTGGCA 10142
 QY 718 ACATGGTGAACCTGTCTACTAAATAACAAATAATAGCCAGCACAGTGTGTCAC 777
 Db 10141 ACATGGTGAACCTGTCTACTAAATAACAAATAATAGCTGGCGTGTGTCATGCAC 10082
 QY 778 TGGTAGTCCAGTACTCGGAGCTACCTGAGATCAGGAGTCAGGAGTCAGGAGTCAGCA 837
 Db 10081 CTATTAATCCAGTACTCGGAGCTACCTGAGATCAGGAGTCAGGAGTCAGGAGTCAGCA 10022
 QY 838 CGTGGCGGTGAGCGAGATGCGCGCTGATTCAGCCCTGGGACAAGAGTGACTCC 897
 Db 10021 GGTGCGAGTCAGGAGTCAGCCACTCAGCTGGGACAAGAGTGACTCC 9962
 QY 898 ATCTCACACA 907
 Db 9961 GTCTCAAAA 9952

RESULT 13
 US-09-949-016-16757/C
 Sequence 16758, Application US/09949016
 Patent No. 6812339

GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 16758
 LENGTH: 35678
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-16757

Query Match 23.1%; Score 209.2; DB 4; Length 35678;
 Best Local Similarity 79.7%; Pred. No. 4e-54; Mismatches 63; Indels 0; Gaps 0;
 Matches 247; Conservative 0; N mismatches 0;

QY 598 ATTAGCAATTAAACTGAGAATGGCGGGACGGTGTGCTAACGCCCTGTAATCCAGCA 657
 Db 10261 ATATGTTAAATAATAGAGAGCAGGAGCTGGCACAGTGCTATGCTTATATCCAGCA 10202
 Db 10201 CTTTGGGAGGCCGAGGGGGTGTGATCAGCTGAGATCAGGAGTCAGCCAGCTGGCA 10142
 QY 718 ACATGGTGAACCTGTCTACTAAATAACAAATAATAGCCAGCACAGTGTGTCAC 777
 Db 10141 ACATGGTGAACCTGTCTACTAAATAACAAATAATAGCTGGCGTGTGTCATGCAC 10082
 QY 778 TGGTAGTCCAGTACTCGGAGCTACCTGAGATCAGGAGTCAGGAGTCAGGAGTCAGCA 837
 Db 10081 CTATTAATCCAGTACTCGGAGCTGAGGAGTCAGCCACTCAGCTGGGACAAGAGTGACTCC 9962
 QY 838 CGTGGCGGTGAGCGAGATGCGCGCTGATTCAGCCCTGGGACAAGAGTGACTCC 897
 Db 10021 GGTGCGAGTCAGGAGTCAGCCACTCAGCTGGGACAAGAGTGACTCC 9962
 QY 898 ATCTCACACA 907
 Db 9961 GTCTCAAAA 9952

RESULT 14
 US-09-949-016-16758/C
 Sequence 16758, Application US/09949016
 Patent No. 6812339

GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 16758
 LENGTH: 35678
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-16757

Query Match 23.1%; Score 209.2; DB 4; Length 35678;
 Best Local Similarity 79.7%; Pred. No. 4e-54; Mismatches 63; Indels 0; Gaps 0;
 Matches 247; Conservative 0; N mismatches 0;

QY 598 ATTAGCAATTAAACTGAGAATGGCGGGACGGTGTGCTAACGCCCTGTAATCCAGCA 657
 Db 10261 ATATGTTAAATAATAGAGAGCAGGAGCTGGCACAGTGCTATGCTTATATCCAGCA 10202
 Db 10201 CTTTGGGAGGCCGAGGGGGTGTGATCAGCTGAGATCAGGAGTCAGCCAGCTGGCA 10142
 QY 718 ACATGGTGAACCTGTCTACTAAATAACAAATAATAGCCAGCACAGTGTGTCAC 777
 Db 10141 ACATGGTGAACCTGTCTACTAAATAACAAATAATAGCTGGCGTGTGTCATGCAC 10082
 QY 778 TGGTAGTCCAGTACTCGGAGCTACCTGAGATCAGGAGTCAGGAGTCAGGAGTCAGCA 837
 Db 10081 CTATTAATCCAGTACTCGGAGCTGAGGAGTCAGCCACTCAGCTGGGACAAGAGTGACTCC 9962
 QY 838 CGTGGCGGTGAGCGAGATGCGCGCTGATTCAGCCCTGGGACAAGAGTGACTCC 897
 Db 10021 GGTGCGAGTCAGGAGTCAGCCACTCAGCTGGGACAAGAGTGACTCC 9962
 QY 898 ATCTCACACA 907
 Db 9961 GTCTCAAAA 9952

RESULT 15
 US-09-949-016-16755/C
 Sequence 16755, Application US/09949016
 Patent No. 6812339

GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307

```

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: fastSEQ for Windows Version 4.0
; SEQ ID NO 16755
; LENGTH: 58361
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16755

```

```

Query Match          23.1%; Score 209.2; DB 4; Length 58361;
Best Local Similarity 79.7%; Conservative 0; Pred. No. 5.2e-54;
Matches 247; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
Qy      598 ATTTAGCAATTAACTGAGAAATGGCGCGGACGGTGGCTACGCCTGTATCCAGCA 657
Db      32944 ATATGTAATTAAATAATAGAGCAGCAGCTATGCTTATATCCAGCA 32885
Qy      658 CTTTGGGGCCGGGGGGGGATCACCTGAGATCAGGAGTCAGACCACCTGCCA 717
Db      32884 CTTTGGAAGGGCGAGGGGGTGGATCACTTGAGTCAGGAGTCAGACCCCTGCCA 32825
Qy      718 AGATGGTGAACCTGTACTAAATAACAAAATTAGCAGGCAAGTGTGTCAC 777
Db      32824 AATGGTGAACCTGTACTAAATAACAAAATTAGCAGGCAAGTGTGTCAC 32765
Qy      778 TCGTAGTCCAGCTACTGGGGCTGAGGCGGAATCGCTTGAAACCCAGGCGGA 837
Db      32764 CTATAATCCACGCTACTGGGGCTGAGGAGATCACTGGAAACCCAGGCGGA 32705
Qy      838 CGTTGGCGTGGACCGAGATGGCGCGTGTTCAGGCTGGCGACAGAGTGAGCTC 897
Db      32704 GGTTGCACTGAGCTGAGATCAGCCACTCCACGCTGGTACAGAGTCAGCT 32645
Qy      898 ATCTCACACA 907
Db      32644 GTCCTCAAAA 32635

```

Search completed: September 15, 2005, 18:28:34
 Job time : 327 Secs

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OM nucleic - nucleic search, using sw model
Run on: September 15, 2005, 15:56:28 ; Search time 3740 Seconds
(without alignments)
9231.094 Million cell updates/sec

Title: US-09-989-733-398

Perfect score: 907

Sequence: 1 ggactctgaaaggcccaagg.....gtgagactccatctcacaca 907

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : EST,*
1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

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6: gb_est5:*

7: gb_est6:*

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9: gb_gis2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match Length	DB ID	Description
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C	2	470	51.8	2	BPF14480	BPF14480 IL3-UT011
C	3	470	51.8	2	BPF15910	BPF15910 IL3-UT011
C	4	469	51.7	2	BPF12836	BPF12836 IL3-UT011
C	5	466.4	51.4	6	CBP85553	CBP85553 AGNCOURT
C	6	458	480	1	AA6464988	AA6464988 zzzba0a06.r
C	7	403	44.4	1	AA293138	AA293138 zzzb605.r
C	8	369	40.7	1	AA299124	AA299124 zzzga02.r
C	9	344.2	37.9	3	AA481156	AA481156 zzz4d03.r
C	10	334.4	36.9	4	BMP854082	K-EST0136
C	11	308	34.0	5	BPF63567	BPF63567 PMI-NN120
C	12	308	34.0	4	B1034628	B1034628 PMI-NN120
C	13	304.8	33.6	7	CN277578	CN277578 17005001
C	14	281.4	31.0	1	AL133867	AL133867 DKE2P763H
C	15	271.1	29.9	3	BPF128767	BPF128767 PMI-MTO19
C	16	238.2	26.3	4	AV710673	AV710673 AV710673
C	17	233.4	25.7	5	BG95746	BG95746 MR2-HTM16
C	18	231.6	25.5	4	BPF95902	BPF95902 PMI-NN120
C	19	228.8	25.2	2	BPF93567	BPF93567 602081954
C	20	222	24.5	1	BMP47000	BMP4700 AGENCOURT
C	21	215	23.7	2	BPF12829	BPF12829 IL3-UT011
C	22	212	23.4	6	BX483243	BX483243 CB70005
C	23	211.2	23.3	5	BX483243	BX483243 DKE2P665G
C	24	210.8	23.2	5	BP320355	BP320355

C	25	209.2	23.1	481	6	CA391442 CB15009.Y
C	26	208.6	23.0	640	8	AZ519506 RPC111-3
C	27	208.4	23.0	692	1	AV70758 AV70758
C	28	207.8	22.9	413	7	AV76406 AV76406
C	29	207.8	22.9	490	7	H59511 YF3-5C02.r1
C	30	207.8	22.9	521	8	AQ784619 HS 3248A
C	31	207.4	22.9	398	5	BX484839 DKFZ2686K
C	32	207.2	22.8	313	1	AA82565 BX484839
C	33	207.2	22.8	571	4	BT25712 60296092
C	34	206.8	22.8	692	9	AG16921 Pan trogl
C	35	206.4	22.8	645	9	AG064993 Pan trogl
C	36	206.2	22.7	583	5	BX494015 BX494015
C	37	205.8	22.7	274	4	BX4957905 PML-RN120
C	38	205.8	22.7	558	4	BW66389 UI-E-CQ1-
C	39	205.8	22.7	584	1	BP301691 BP301691
C	40	205	22.6	488	1	AR70562 NW21101.S
C	41	205	22.6	745	8	AQ72732 HS 5268B
C	42	205	22.6	1500	3	BC021103 Homo sapi
C	43	204.6	22.6	514	8	B51474 C1T978SR-A-
C	44	204.6	22.6	810	4	BF968874 B998874
C	45	204.4	22.5	429	7	CN264016 17005000
C	46	204.4	22.5	487	7	CN275741 17005000
C	47	204.4	22.5	686	4	BG819887 602781970
C	48	204.4	22.5	687	3	BC09875 Homo sapi
C	49	204.4	22.5	402	5	BQ631269 W02419
C	50	204	22.5	429	2	BQ501670 BQ501670
C	51	204	22.5	57	5	BQ790005 In49d06.x
C	52	204	22.5	58	5	AQ310879 CIT-RSP-2
C	53	204	22.5	59	5	AQ316800 RCP11-3P
C	54	203.8	22.5	392	7	AG088570 Pan trogl
C	55	203.8	22.5	399	7	BQ271642 ik16e10.x
C	56	203.8	22.5	429	2	W02419 zzz1a04.r1
C	57	203.8	22.5	877	5	BQ501670 hz62d07.x
C	58	203.6	22.4	468	1	AL603499 DKE2P86L
C	59	203.6	22.4	866	5	BU12171 PRODGID
C	60	203.6	22.4	984	7	BU07135 AGNCOURT
C	61	203.6	22.4	456	5	CR749501 Homo sapi
C	62	203.2	22.4	643	9	AG129001 Pan trogl
C	63	203.2	22.4	670	4	BM671184 UI-E-CQ1-
C	64	203	22.4	321	5	AW511569 xu6a07.x
C	65	203	22.3	738	9	AG181502 Pan trogl
C	66	202.8	22.4	445	7	BB140949 MR0-HT06
C	67	202.8	22.4	462	5	BQ438489 AGNCOURT
C	68	202.8	22.4	823	8	AQ741080 HS 2172A
C	69	202.6	22.3	393	7	HM8293 YR2F07..R1
C	70	202.6	22.3	444	5	BM92670 UI-H-DPO-
C	71	202.6	22.3	530	5	BX283237 BX283237
C	72	202.6	22.3	687	9	AG123074 Pan trogl
C	73	202.6	22.3	719	4	BM679548 UI-E-SO0-
C	74	202.6	22.3	817	2	BB747923 60158082
C	75	202.6	22.3	973	5	BX435546 BX435546
C	76	202.6	22.3	3443	3	All36891 Homo sapi
C	77	202.6	22.3	7004	3	CR749209 Homo sapi
C	78	202.4	22.3	556	7	CK822725 1997a04Y
C	79	202.4	22.3	447	2	BP901147 IL2-MT017
C	80	202.2	22.3	498	7	CR542874 DKE2P849M
C	81	202.2	22.3	586	5	CA406158 10023079
C	82	202.2	22.3	633	5	BM977586 UI-CF-RN1
C	83	202.2	22.3	696	9	BM971480 UI-FC-BE1
C	84	202.2	22.3	701	9	AG170941 Pan trogl
C	85	202.2	22.3	799	6	CD655686 AGNCOURT
C	86	202.2	22.3	924	5	BQ710195 AGNCOURT
C	87	202.2	22.3	320	5	BUS88558 AGNCOURT
C	88	202	22.3	588	8	AQ3173949 RCP11-15
C	89	202	22.3	661	9	AG059678 Pan trogl
C	90	202	22.3	673	9	AQ317551 RCP11-15
C	91	201.8	22.2	455	8	CA391442 CB15009.Y
C	92	201.6	22.2	498	8	AQ479702 RCP11-12
C	93	201.6	22.2	560	8	AQ479619 RCP11-12
C	94	201.6	22.2	649	9	AG064566 Pan trogl
C	95	201.6	22.2	1998	3	CR623156 Full-1leng
C	96	201.4	22.2	383	7	AI369076 QV29h03.x
C	97	201.4	22.2	394	7	CN278335 170006002

C	98	201.4	22.2	652	8	AQ266609	RPC11-75	171	199.2	22.0	577	8	AQ483173
C	99	201.4	22.2	683	9	AG177245	Pan trogl	172	199.2	22.0	579	7	CR545097
C	100	201.4	22.2	894	8	AG173871	HS_5302_B	173	199.2	22.0	635	7	CR545097
C	101	201.2	22.2	368	1	AG623009	NP79H05_B	174	199.2	22.0	657	9	AG150142
C	102	201.2	22.2	417	1	AV733634		175	199.2	22.0	674	7	CN341729
C	103	201.2	22.2	420	2	AQ36829	CIT-HSP-2	176	199.2	22.0	688	7	CR76437
C	104	201.2	22.2	494	8	AQ228611	AQ228611_HB_2009_A	177	199	21.9	370	8	AQ263765
C	105	201.2	22.2	533	7	CN480174	UI-H-BUO-	178	199	21.9	559	1	AU15806
C	106	201.2	22.2	618	6	CA33336	NISC_It9	179	199	21.9	612	5	BUR952525
C	107	201.2	22.2	680	5	BX114339		180	199	21.9	617	8	AQ191717
C	108	201.2	22.2	1548	3	CR594735	CIT-HSP-2	181	199	21.9	649	5	BM991864
C	109	201	22.2	485	8	B69763	B69763_CIT-HSP-2	182	199	21.9	724	8	BZ612696
C	110	201	22.2	652	5	BX951325	BX951325_DKFZP781M	183	198.8	21.9	374	1	AJ128479
C	111	201	22.2	750	9	AG081408	Pan trogl	184	198.8	21.9	392	8	AQ47283
C	112	201	22.2	938	8	AP101690	AP101690	185	198.8	21.9	472	5	CD370173
C	113	200.8	22.1	353	7	CN271795		186	198.8	21.9	769	6	AW177869
C	114	200.8	22.1	372	7	BW991270	UI-H-DIO-	187	198.8	21.9	897	8	AQ74210
C	115	200.8	22.1	723	7	CR789995	DKFZP459P	188	198.8	21.9	921	5	BK770271
C	116	200.8	22.1	854	6	CD171905	CD171905_AGENCOURT	189	198.6	21.9	349	7	T03928
C	117	200.8	22.1	795	5	BX333363	BX333363	190	198.6	21.9	349	7	T24036
C	118	200.6	22.1	449	2	BB042511	BB042511_ho23B017.x	191	198.6	21.9	354	4	BW662676
C	119	200.6	22.1	485	8	AQ219222	AQ219222_HS_325_B	192	198.6	21.9	515	2	AN177869
C	120	200.6	22.1	503	4	BW510027	BW510027_1997aB4.x	193	198.6	21.9	548	7	CN414083
C	121	200.6	22.1	808	4	BG622731	BG622731_WHACH59TR	194	198.6	21.9	679	2	BE322753
C	122	200.6	22.1	785	5	BUS67231	BUS67231_AGENCOURT	195	198.6	21.9	694	6	CA420398
C	123	200.6	22.1	799	1	AV693410	BB854310	196	198.6	21.9	369	4	BW671251
C	124	200.4	22.1	360	1	A1254267	A1254267_QV4-BT025	197	198.4	21.9	390	5	T24136
C	125	200.4	22.1	507	1	AA601712	AA601712_no3a05.8	198	198.4	21.9	426	7	BN252500
C	126	200.4	22.1	687	9	AG135036	Pan trogl	199	198.4	21.9	664	7	CN35233
C	127	200.4	22.1	744	7	CR791150	CR791150_DKFZP469B	200	198.4	21.9	914	5	AW32831
C	128	200.4	22.1	1750	3	AP119908	AP119908_Homo_bapi	201	198.4	21.9	922	5	BW562331
C	129	200.2	22.1	416	1	AV693356	AV693356_AGENCOURT	202	198.2	21.9	324	4	CD370173
C	130	200.2	22.1	420	5	BB06245	BB06245_QV4-BT025	203	198.2	21.9	404	8	BM61251
C	131	200.2	22.1	421	1	AV691556	AV691556_AV691556	204	198.2	21.9	453	8	AN177869
C	132	200.2	22.1	569	1	AG102562	AG102562_Pan trogl	205	198.2	21.9	493	2	CN414083
C	133	200.2	22.1	654	7	CR791150	CR791150_DKFZP469B	206	198.2	21.9	504	4	BW322753
C	134	200.2	22.1	690	4	BP971234	BP971234_602273252	207	198.2	21.9	510	1	AV75056
C	135	200.2	22.1	1034	4	BB060909	BB060909_AGENCOURT	208	198.2	21.9	562	7	CA420398
C	136	200.2	22.1	557	5	BM991139	BM991139_U1-H-DIO-	209	198.2	21.9	580	5	CK818567
C	137	200	22.1	586	5	BX951238	BX951238_DKFZP781P	210	198.2	21.9	648	8	BP26216
C	138	200	22.1	621	9	AG102562	AG102562_Pan trogl	211	198.2	21.9	669	5	AN177869
C	139	200	22.1	665	9	AG045689	AG045689_Pan trogl	212	198.2	21.9	679	9	CD370173
C	140	199.8	22.0	439	1	AI355559	AI355559_QT75105.x	213	198.2	21.9	681	9	AW32831
C	141	199.8	22.0	466	8	AQ483846	AQ483846_RPC1-11.x	214	198.2	21.9	716	9	BM61251
C	142	199.8	22.0	564	6	CN413054	CN413054_17005326	215	198.2	21.9	1238	4	AN177869
C	143	199.8	22.0	581	2	AW970987	AW970987_EST3B3072	216	198.2	21.9	386	7	CD370173
C	144	199.8	22.0	595	8	AQ424774	AQ424774_CIT-B1-EI-	217	198.2	21.9	387	5	AW32831
C	145	199.8	22.0	730	5	BU616124	BU616124_UI-H-DFO-	218	198.2	21.9	493	5	BM61251
C	146	199.8	22.0	837	5	BX486445	BX486445_DKFZP6860	219	198.2	21.9	504	9	CD370173
C	147	199.8	22.0	840	1	AL706641	AL706641_DKFZP86B	220	198.2	21.9	636	5	AG002485
C	148	199.8	22.0	919	3	BC013247	BC013247_Homo_bapi	221	198.2	21.9	657	8	BM455282
C	149	199.8	22.0	960	6	CD245816	CD245816_AGENCOURT	222	198.2	21.9	887	5	CD370173
C	150	199.6	22.0	357	1	AI031759	AI031759_OW39d11.x	223	198.2	21.9	919	5	CD370173
C	151	199.6	22.0	423	8	AQ059624	AQ059624_CIT-HSP-2	224	197.8	21.8	493	5	CD370173
C	152	199.6	22.0	458	2	AW151247	AW151247_xg3404-x.x	225	197.8	21.8	493	5	CD370173
C	153	199.6	22.0	572	8	AQ763732	AQ763732_HS_3186_A	226	197.8	21.8	442	2	CD370173
C	154	199.6	22.0	680	5	BN995796	BN995796_UT-H-BDO-	227	197.8	21.8	467	8	CD370173
C	155	199.6	22.0	681	5	BQ016777	BQ016777_UT-H-DIO-	228	197.8	21.8	475	2	CD370173
C	156	199.6	22.0	684	5	BQ772479	BQ772479_UT-H-FBO-	229	197.8	21.8	478	7	CD370173
C	157	199.6	22.0	736	5	BQ004411	BQ004411_UT-H-DPO-	230	197.8	21.8	549	6	CD370173
C	158	199.6	22.0	862	4	BG762519	BG762519_602733970	231	197.8	21.8	551	6	CD370173
C	159	199.6	22.0	876	6	CD556766	CD556766_AGENCOURT	232	197.8	21.8	583	5	CD370173
C	160	199.6	22.0	909	4	BG034698	BG034698_60230050	233	197.8	21.8	590	8	CD370173
C	161	199.6	22.0	941	5	BX451504	BX451504_BX451504	234	197.8	21.8	664	7	CD370173
C	162	199.6	22.0	3128	3	CR627380	CR627380_Homo_bapi	235	197.8	21.8	672	5	CD370173
C	163	199.6	22.0	3243	3	HSM803448	HSM803448	236	197.8	21.8	699	5	CD370173
C	164	199.4	22.0	321	5	BUS958280	BUS958280_AGENCOURT	237	197.6	21.8	350	1	CD370173
C	165	199.4	22.0	379	8	AQ580711	AQ580711_RPC1-11.x	238	197.6	21.8	453	5	CD370173
C	166	199.4	22.0	558	5	BUS80548	BUS80548_in35c05.x	239	197.6	21.8	479	1	CD370173
C	167	199.4	22.0	604	6	BW990713	BW990713_UT-H-DIO-	240	197.6	21.8	662	9	CD370173
C	168	199.4	22.0	622	9	AG050042	AG050042_Pan trogl	241	197.6	21.8	707	5	CD370173
C	169	199.4	22.0	4974	3	AL833737	AL833737_Homo_bapi	242	197.6	21.8	843	5	CD370173
C	170	199.2	22.0	427	1	A1123488	A1123488_qa01f01.x	243	197.6	21.8	957	5	CD370173

C	244	197.6	21.8	993	3	AF318326		317	196.6	21.7	592	5	BP267287		BP267287	
C	245	197.6	21.8	3204	3	HSM84305		318	196.6	21.7	582	5	BP25852		BP25852	
C	246	197.6	21.8	5093	3	HSM809153		319	196.6	21.7	582	5	BP292016		BP292016	
C	247	197.4	21.8	324	1	A124108		320	196.6	21.7	583	5	BP268005		BP268005	
C	248	197.4	21.8	330	5	BUS56193		322	196.6	21.7	596	5	BX84036		DKE22686N	
C	249	197.4	21.8	344	1	A1590404		323	196.6	21.7	601	1	AL708507		AL708507	
C	250	197.4	21.8	401	8	AQ669103		323	196.6	21.7	635	8	AQ313550		AQ313550	
C	251	197.4	21.8	492	5	BQ706631		324	196.6	21.7	637	4	BM631791		BM631791	
C	252	197.4	21.8	541	5	BW931720		325	196.6	21.7	645	7	CN362346		CN362346	
C	253	197.4	21.8	594	5	BX49380		326	196.6	21.7	652	9	AG16098		Pan_trogl	
C	254	197.4	21.8	613	5	BW90533		327	196.6	21.7	661	2	BE177530		BE177530	
C	255	197.4	21.8	677	7	CR04046		328	196.6	21.7	701	7	CF125387		CF125387	
C	256	197.4	21.8	723	9	AG14729		329	196.6	21.7	777	4	BI033486		BI033486	
C	257	197.4	21.8	733	6	CA308850		330	196.6	21.7	824	8	BZ611785		WHACP33TR	
C	258	197.4	21.8	902	2	BP034649		331	196.6	21.7	879	3	CR14544		BX14544	
C	260	197.4	21.8	949	5	BQ950110		332	196.6	21.7	1000	5	BQ049398		BQ049398	
C	261	197.4	21.7	379	1	AV68406		333	196.6	21.7	1023	4	BM424942		BM424942	
C	262	197.2	21.7	642	7	CN270868		334	196.6	21.7	1143	1	BM918656		BM918656	
C	263	197.2	21.7	412	8	AZ518582		335	196.6	21.7	1359	8	AF101912		AF101912	
C	264	197.2	21.7	420	1	A1760355		336	196.6	21.7	1588	3	CR556829		CR556829	
C	265	197.2	21.7	477	1	AT92635		337	196.6	21.7	3535	1	BH09896		HIV2C03	
C	266	197.2	21.7	516	8	AQ691270		338	196.6	21.7	3974	3	HSM805841		BX337757	
C	267	197.2	21.7	642	7	BM008851		339	196.6	21.7	4747	3	HSMW00875		BQ49398	
C	268	197.2	21.7	644	8	AD404535		340	196.4	21.7	498	2	AW212513		AW212513	
C	269	197.2	21.7	751	1	A118382		341	196.4	21.7	498	8	AQ632383		AQ632383	
C	270	197.2	21.7	784	1	A1521360		342	196.4	21.7	498	8	CD706660		CD706660	
C	271	197.2	21.7	399	4	BG223374		343	196.4	21.7	498	8	AI521360		AI521360	
C	272	197.2	21.7	417	1	AV697609		344	196.4	21.7	498	8	BC018955		BC018955	
C	273	197.2	21.7	574	9	CR559874		345	196.4	21.7	498	8	B36003		B36003	
C	274	197.2	21.7	633	9	AG14698		346	196.4	21.7	498	8	BU333187		BU333187	
C	275	197.2	21.7	635	7	CR768142		347	196.2	21.6	567	5	AA503307		AA503307	
C	276	197.2	21.7	741	8	A2517850		348	196.2	21.6	568	2	BB320286		BB320286	
C	277	197.2	21.7	770	5	BX090291		349	196.2	21.6	569	2	CD706660		CD706660	
C	278	197.2	21.7	775	4	BB867712		350	196.2	21.6	570	2	BP0342192		BP0342192	
C	279	197.2	21.7	826	5	BQ436665		351	196.2	21.6	570	2	BP267172		BP267172	
C	280	197.2	21.7	866	5	BQ712664		352	196.2	21.6	570	2	RC55-018		RC55-018	
C	281	197.2	21.7	884	5	BQ71287		353	196.2	21.6	570	2	BE28286		BE28286	
C	282	197.2	21.7	893	5	BQ706660		354	196.2	21.6	570	2	CD706660		CD706660	
C	283	197.2	21.7	900	5	BB886692		355	196.2	21.6	570	2	BP267172		BP267172	
C	284	197.2	21.7	903	2	BB867712		356	196.2	21.6	570	2	CD706660		CD706660	
C	285	197.2	21.7	975	3	CR627381		357	196.2	21.6	570	2	AAU44397		AAU44397	
C	286	197.2	21.7	323	1	AT774223		358	196.2	21.6	570	2	BP267172		BP267172	
C	287	197.2	21.7	342	1	A1174703		359	196.2	21.6	570	2	AWB13106		AWB13106	
C	288	197.2	21.7	390	1	AM719543		360	196.2	21.6	570	2	CN840509		CN840509	
C	289	197.2	21.7	416	1	BB062476		361	196.2	21.6	570	2	AI501563		AI501563	
C	290	197.2	21.7	433	8	AQ342192		362	196.2	21.6	570	2	BP0342192		BP0342192	
C	291	197.2	21.7	439	4	CR172488		363	196.2	21.6	570	2	CD706660		CD706660	
C	292	197.2	21.7	477	1	AT709726		364	196.2	21.6	570	2	BP267172		BP267172	
C	293	197.2	21.7	478	1	AT761677		365	196.2	21.6	570	2	CD706660		CD706660	
C	294	197.2	21.7	483	8	AQ829636		366	196.2	21.6	570	2	BP267172		BP267172	
C	295	197.2	21.7	504	5	BP490571		367	196.2	21.6	570	2	CD706660		CD706660	
C	296	197.2	21.7	532	4	BG830539		368	196.2	21.6	570	2	BP267172		BP267172	
C	297	197.2	21.7	572	4	BR743761		369	196.2	21.6	570	2	CD706660		CD706660	
C	298	197.2	21.7	587	1	BR261089		370	196.2	21.6	570	2	BP267172		BP267172	
C	299	197.2	21.7	604	1	AV729714		371	196.2	21.6	570	2	CD706660		CD706660	
C	300	197.2	21.7	685	7	CK01797		372	196.2	21.6	570	2	BP267172		BP267172	
C	301	197.2	21.7	709	5	BR67938		373	196.2	21.6	570	2	CD706660		CD706660	
C	302	197.2	21.7	718	8	BG773121		374	196.2	21.6	570	2	BP267172		BP267172	
C	303	197.2	21.7	730	3	CR615928		375	196.2	21.6	570	2	CD706660		CD706660	
C	304	197.2	21.7	757	1	BR261089		376	196.2	21.6	570	2	BP267172		BP267172	
C	305	197.2	21.7	5641	3	HEM806468		377	196.2	21.6	570	2	CD706660		CD706660	
C	306	197.2	21.7	313	4	BW710087		378	196.2	21.6	570	2	BP267172		BP267172	
C	307	197.2	21.7	352	1	A157280		379	196.2	21.6	570	2	CD706660		CD706660	
C	308	197.2	21.7	380	2	BR246411		380	196.2	21.6	570	2	BP267172		BP267172	
C	309	197.2	21.7	400	4	BR260612		381	196.2	21.6	570	2	CD706660		CD706660	
C	310	197.2	21.7	426	1	AT914748		382	196.2	21.6	570	2	BP267172		BP267172	
C	311	197.2	21.7	436	2	BP816190		383	196.2	21.6	570	2	CD706660		CD706660	
C	312	197.2	21.7	461	3	AM151848		384	196.2	21.6	570	2	BP267172		BP267172	
C	313	197.2	21.7	491	2	BR639303		385	196.2	21.6	570	2	CD706660		CD706660	
C	314	197.2	21.7	493	1	AT733523		386	196.2	21.6	570	2	BP267172		BP267172	
C	315	197.2	21.7	578	5	BP267532		387	196.2	21.6	570	2	CD706660		CD706660	
C	316	197.2	21.7	579	5	BP266615		388	196.2	21.6	570	2	CD706660		CD706660	

C 390	195.6	21.6	441	8	AZ521019	C 463	195	21.5	680	9	AG077619
C 391	195.6	21.6	480	7	CN269107	C 464	195	21.5	682	9	AG181743
C 392	195.6	21.6	500	8	AQ428325	C 465	195	21.5	705	7	CN278633
C 393	195.6	21.6	521	5	BUE11227	C 466	195	21.5	769	5	BUE54207
C 394	195.6	21.6	529	8	B92837	C 467	195	21.5	792	1	AU136365
C 395	195.6	21.6	566	1	BUE73318	C 468	195	21.5	885	8	AQ739135
C 396	195.6	21.6	573	2	AW97923	C 469	195	21.5	886	8	AQ739494
C 397	195.6	21.6	580	1	AU150583	C 470	195	21.5	910	5	BUB50247
C 398	195.6	21.6	580	8	BP334328	C 471	195	21.5	915	5	BUI149187
C 399	195.6	21.6	580	5	BQ053726	C 472	195	21.5	924	4	BG697612
C 400	195.6	21.6	598	1	BQ011808	C 473	195	21.5	998	5	BX81716
C 401	195.6	21.6	609	9	AG149236	C 474	195	21.5	1007	8	BZ611150
C 402	195.6	21.6	616	5	BUE17236	C 475	195	21.5	1035	5	BQ17751
C 403	195.6	21.6	619	8	B58514	C 476	195	21.5	1769	3	AF130079
C 404	195.6	21.6	660	8	CR54328	C 477	195	21.5	1850	5	BC025771
C 405	195.6	21.6	684	8	AQ632073	C 478	194.8	21.5	340	1	AA66625
C 406	195.6	21.6	702	9	AG153097	C 479	194.8	21.5	383	1	AV55252
C 407	195.6	21.6	729	7	CN302098	C 480	194.8	21.5	394	1	AT732690
C 408	195.6	21.6	731	1	AI687343	C 481	194.8	21.5	420	1	AA67912
C 409	195.6	21.6	791	5	BUR94219	C 482	194.8	21.5	434	1	AA487569
C 410	195.6	21.6	836	2	CR771122	C 483	194.8	21.5	438	1	AT702018
C 411	195.6	21.6	977	3	CR600792	C 484	194.8	21.5	457	8	AQ319790
C 412	195.6	21.6	1111	5	BK437747	C 485	194.8	21.5	532	1	ALU36896
C 413	195.6	21.6	342	5	BX480789	C 486	194.8	21.5	547	8	AQ046948
C 414	195.6	21.5	352	1	AT701898	C 487	194.8	21.5	553	1	AU158457
C 415	195.6	21.5	421	1	AI473671	C 488	194.8	21.5	643	9	AG04162
C 416	195.6	21.5	427	2	AWB80986	C 489	194.8	21.5	658	9	AG054232
C 417	195.6	21.5	439	8	AQ768011	C 490	194.8	21.5	658	9	AG151757
C 418	195.6	21.5	450	7	T51920	C 491	194.8	21.5	713	8	AQ546618
C 419	195.6	21.5	505	7	BX952682	C 492	194.8	21.5	825	8	AG462661
C 420	195.6	21.5	505	8	AQ477081	C 493	194.8	21.5	943	8	AT0743038
C 421	195.6	21.5	510	5	BUS90031	C 494	194.8	21.5	1107	7	BX338918
C 422	195.6	21.5	528	7	CB263175	C 495	194.8	21.5	6789	3	AT1702018
C 423	195.6	21.5	578	7	CK818107	C 496	194.8	21.5	398	1	AT1798521
C 424	195.6	21.5	586	1	AI207422	C 497	194.6	21.5	440	8	AQ027499
C 425	195.6	21.5	615	8	AQ345915	C 498	194.6	21.5	449	8	AT062661
C 426	195.6	21.5	714	9	AG122688	C 499	194.6	21.5	487	8	B55517
C 427	195.6	21.5	359	7	F2338	C 500	194.6	21.5	508	8	AQ125893
C 428	195.6	21.5	360	6	CI4614	C 501	194.6	21.5	535	8	AQ395337
C 429	195.6	21.5	385	6	CB296760	C 502	194.6	21.5	539	8	AQ544113
C 430	195.6	21.5	405	1	AI280535	C 503	194.6	21.5	619	7	CF146583
C 431	195.6	21.5	615	8	BX116453	C 504	194.6	21.5	658	9	AG087949
C 432	195.6	21.5	437	5	BX489723	C 505	194.6	21.5	664	1	AL120004
C 433	195.6	21.5	443	8	AQ436649	C 506	194.6	21.5	669	5	BX951401
C 434	195.6	21.5	448	8	BQ503175	C 507	194.6	21.5	675	5	BW919176
C 435	195.6	21.5	503	1	AA60149	C 508	194.6	21.5	1077	5	AT1798521
C 436	195.6	21.5	542	5	BQ001553	C 509	194.6	21.5	704	7	CF122920
C 437	195.6	21.5	543	1	AA019919	C 510	194.6	21.5	359	8	AT0759354
C 438	195.6	21.5	552	2	AW970588	C 511	194.6	21.5	708	9	AG154962
C 439	195.6	21.5	602	5	BUE57458	C 512	194.6	21.5	712	9	AG095201
C 440	195.6	21.5	633	9	AG094873	C 513	194.6	21.5	877	5	AT1798521
C 441	195.6	21.5	656	4	BG98542	C 514	194.6	21.5	1077	5	AT1798521
C 442	195.6	21.5	660	9	AG011123	C 515	194.6	21.5	1210	1	CF122920
C 443	195.6	21.5	543	1	AA019919	C 516	194.6	21.4	359	8	AG085420
C 444	195.6	21.5	704	9	AG011528	C 517	194.4	21.4	366	1	AT1283938
C 445	195.6	21.5	769	8	AQ900076	C 518	194.4	21.4	392	1	AT311796
C 446	195.6	21.5	951	5	BQ710495	C 519	194.4	21.4	402	4	BG21988
C 447	195.6	21.5	1758	3	BC004550	C 520	194.4	21.4	412	2	BR062478
C 448	195.6	21.5	393	8	BBF05088	C 521	194.4	21.4	427	2	AW272815
C 449	195.6	21.5	393	8	AQ771301	C 522	194.4	21.4	432	8	AT0759354
C 450	195.6	21.5	704	1	AI26818	C 523	194.4	21.4	436	1	AT1283938
C 451	195.6	21.5	447	1	AI281622	C 524	194.4	21.4	439	1	AT311796
C 452	195.6	21.5	459	7	BPX81314	C 525	194.4	21.4	523	4	BP04793
C 453	195.6	21.5	468	7	CN349180	C 526	194.4	21.4	526	7	BQ422406.X
C 454	195.6	21.5	398	1	CK824505	C 527	194.4	21.4	527	7	CR59366
C 455	195.6	21.5	527	7	CR54971	C 528	194.4	21.4	635	7	CR629762
C 456	195.6	21.5	527	8	AQ466047	C 529	194.4	21.4	647	8	AT1283938
C 457	195.6	21.5	530	1	BPX81314	C 530	194.4	21.4	672	9	AG066531
C 458	195.6	21.5	559	7	CN349183	C 531	194.4	21.4	681	9	AG182173
C 459	195.6	21.5	566	5	BP266899	C 532	194.4	21.4	686	9	AG117862
C 460	195.6	21.5	624	2	BX509953	C 533	194.4	21.4	688	9	AG182171
C 461	195.6	21.5	640	7	CF128614	C 534	194.4	21.4	699	4	BG570479
C 462	195.6	21.5	640	7	CF128614	C 535	194.4	21.4	700	5	CN270895

C	536	194.4	21.4	826	5	BQ220083	AGENCOURT	C	609	194	21.4	1613	3	CR591695	full-leng
C	537	194.4	21.4	907	5	BQ710503	AGENCOURT	C	610	193.8	21.4	263	4	BI007641	MRA-RTO4
C	538	194.4	21.4	916	4	BP983617	AGENCOURT	C	611	193.8	21.4	409	1	AA767592	AG980707-8
C	539	194.4	21.4	985	5	BUS87770	AGENCOURT	C	612	193.8	21.4	426	2	AW771062	HS-51d09_x
C	540	194.4	21.4	320	5	BUS87770	AGENCOURT	C	613	193.8	21.4	441	2	BP738059	BP738059
C	541	194.2	21.4	354	8	AQ277656	CITB1-E1-	C	614	193.8	21.4	469	5	CD691341	BS77864_h
C	542	194.2	21.4	368	7	N23099	Yw43906-81	C	615	193.8	21.4	486	6	CA848153	IP34610_x
C	543	194.2	21.4	421	8	AQ066554	HS_2210_A	C	616	193.8	21.4	495	8	B33673	BJ33673 HS-_0223-A1
C	544	194.2	21.4	433	6	CD23813	FNPAPH01	C	617	193.8	21.4	521	8	AQ777326	AQ777326 HS_2247_B
C	545	194.2	21.4	434	1	AA05647	z177qd03_s	C	618	193.8	21.4	551	2	AW576914	AN576914 RC7-BT031
C	546	194.2	21.4	485	8	AQ135069	AQ135069	C	619	193.8	21.4	616	6	CB67437	CB67437 1q66g12_x
C	547	194.2	21.4	522	8	AQ15894	HS_3082_B	C	620	193.8	21.4	629	9	AG092046	AG092046 Pan_trogl
C	548	194.2	21.4	529	2	AW850230	Tl3-CT021	C	621	193.8	21.4	630	7	CK30112	OJ45c06_Y
C	549	194.2	21.4	533	5	BQ637931	hd16d01_Y	C	622	193.8	21.4	632	6	CA310364	CI310364 UI-H-FTI
C	550	194.2	21.4	560	1	AU15751	AU15751	C	623	193.8	21.4	646	8	AQ313437	AQ313437 RCP111-10
C	551	194.2	21.4	573	1	AU117849	AU117849	C	624	193.8	21.4	656	4	BG571155	BG571155 602574359
C	552	194.2	21.4	579	2	BH143664	MRO-HT016	C	625	193.8	21.4	665	9	AG041398	AG041398 Pan_trogl
C	553	194.2	21.4	608	1	ALL70835	AL706835	C	626	193.8	21.4	679	5	BM04233	BM04233 DKFp686C
C	554	194.2	21.4	626	5	BC015077	UI-H-DI0	C	627	193.8	21.4	675	9	AG17725	AG17725 Pan_trogl
C	555	194.2	21.4	634	5	BX480648	BX480648	C	628	193.8	21.4	704	9	AG142906	AG142906 Pan_trogl
C	556	194.2	21.4	690	9	AG185250	Pan_trogl	C	635	193.6	21.4	723	7	FO0688	FO0688 HS322032_S
C	557	194.2	21.4	694	2	CF124970	UI-H-ER01	C	630	193.8	21.4	829	8	AF02038	AF02038
C	558	194.2	21.4	698	5	BQ183396	UI-H-EU0	C	631	193.8	21.4	1053	4	BF970033	BF970033 602272885
C	559	194.2	21.4	707	6	CA439571	UI-H-DI0	C	632	193.8	21.4	1054	5	BM06989	BM06989 AGENCOURT
C	560	194.2	21.4	716	7	CF128414	UI-H-ET0	C	633	193.8	21.4	1077	1	AL524675	AL524675
C	561	194.2	21.4	721	8	AF105676	AF105676	C	634	193.8	21.4	1102	1	AL559764	AL559764
C	562	194.2	21.4	749	8	BZ606363	WHAB133TF	C	635	193.6	21.4	1102	1	AL559764	AL559764
C	563	194.2	21.4	857	5	BUT89543	AGENCOURT	C	636	193.6	21.4	1359	5	BX105637	BX105637
C	564	194.2	21.4	868	6	CDS186945	AGENCOURT	C	637	193.6	21.4	400	8	AQ124663	AQ124663 HS_2267_B
C	565	194.2	21.4	919	4	BPF67724	602287586	C	638	193.6	21.4	409	1	AI287380	AI287380
C	566	194.2	21.4	934	8	BR445249	MR0-HT007	C	639	193.6	21.4	427	8	AQ43288	AQ43288
C	567	194.2	21.4	945	2	AQ125355	HS_2168_A	C	640	193.6	21.4	439	7	F34306	F34306
C	568	194.2	21.4	950	8	AQ727006	HS_5431_A	C	641	193.6	21.4	505	4	AG033142	AG033142
C	569	194.2	21.4	954	8	AQ819451	RCS-ST029	C	642	193.6	21.4	506	8	AQ283914	AQ283914 RCP111-78
C	570	194	21.4	958	1	AG526542	n16010_s	C	643	193.6	21.4	520	7	CN2273753	CN2273753
C	571	194	21.4	964	1	AG194119	Pan_trogl	C	644	193.6	21.4	535	1	AU158095	AU158095 AGENCOURT
C	572	194	21.4	970	8	BR128445	MR0-HT015	C	645	193.6	21.4	543	5	BUT77401	UT-CRF-DU1
C	573	194	21.4	974	1	AV761486	AV761486	C	646	193.6	21.4	585	4	BM045436	BM045436
C	574	194	21.4	978	8	AQ197043	RCS-ST029	C	647	193.6	21.4	589	4	AG019704	AG019704 Homo sapi
C	575	194	21.4	982	8	AB819453	MR3-HN006	C	648	193.6	21.4	661	9	AG033142	AG033142 Pan_trogl
C	576	194	21.4	984	1	AG474083	CITB1-E1-	C	649	193.6	21.4	667	8	AQ194211	AQ194211 RCP111-07_x
C	577	194	21.4	988	8	AQ475209	CITB1-E1-	C	650	193.6	21.4	678	7	AU158095	AU158095 AGENCOURT
C	578	194	21.4	990	4	BR128445	MR0-HT007	C	651	193.6	21.4	680	8	AG484111	AG484111 RCP111-2
C	579	194	21.4	994	2	AQ727006	HS_5431_A	C	652	193.6	21.4	585	4	AV69555	AV69555
C	580	194	21.4	998	6	CD686671	EST3192_h	C	653	193.6	21.4	920	5	BW957399	BW957399 AGENCOURT
C	581	194	21.4	1000	5	AB816648	w104c07_x	C	654	193.6	21.4	920	5	AO780023	AO780023
C	582	194	21.4	1004	1	AU148232	AU148232	C	655	193.6	21.4	1112	1	AQ11398	AQ11398 CITB1-E1-
C	583	194	21.4	1004	5	BP217403	BP217403	C	656	193.6	21.4	763	8	CB310811	CB310811 AGENCOURT
C	584	194	21.4	1006	2	AV966643	EST319217	C	657	193.6	21.4	803	4	BG120824	BG120824
C	585	194	21.4	1006	7	CN479818	UT-H-EU0-h	C	658	193.6	21.4	920	5	BW957399	BW957399 AGENCOURT
C	586	194	21.4	1008	6	CD686671	EST3192_h	C	659	193.6	21.4	920	5	AO780023	AO780023
C	587	194	21.4	1010	5	AB676542	BP335272	C	660	193.6	21.4	388	8	AQ128136	AQ128136 RCP111-14
C	588	194	21.4	1014	1	AU148232	BP217403	C	661	193.6	21.4	413	1	AU161120	AU161120 wh91e03_x
C	589	194	21.4	1014	5	BP220813	BP220813	C	662	193.6	21.4	856	8	AQ125136	AQ125136 HS_2163_B
C	590	194	21.4	1014	7	CN479818	UT-H-EU0-h	C	663	193.6	21.4	920	5	AO780023	AO780023
C	591	194	21.4	1015	6	CD686671	EST3192_h	C	664	193.6	21.4	920	5	AO780023	AO780023
C	592	194	21.4	1015	5	AB676542	BP335272	C	665	193.6	21.4	388	8	AQ128136	AQ128136 RCP111-14
C	593	194	21.4	1015	7	BP217403	BP217403	C	666	193.6	21.4	413	1	AU161120	AU161120 wh91e03_x
C	594	194	21.4	1016	5	AB676542	BP217403	C	667	193.6	21.4	419	1	AU161120	AU161120 wh91e03_x
C	595	194	21.4	1016	7	AU146599	AU146599	C	668	193.6	21.4	450	8	AQ125136	AQ125136 HS_2163_B
C	596	194	21.4	1016	1	AI444575	FLC5007_H	C	669	193.6	21.4	453	1	AU173682	AU173682
C	597	194	21.4	1016	9	AG175061	Pan_trogl	C	670	193.4	21.4	571	7	CK822946	CK822946
C	598	194	21.4	1017	5	CD686671	BP335272	C	671	193.4	21.4	572	5	BPK94125	BPK94125 DKFP7797
C	599	194	21.4	1017	6	AB676542	BP335272	C	672	193.4	21.4	573	8	AQ381570	AQ381570 RCP111-14
C	600	194	21.4	1017	7	BP217403	BP217403	C	673	193.4	21.4	576	5	BK464282	BK464282 DKFP7781H
C	601	194	21.4	1017	9	AB676542	BP335272	C	674	193.4	21.4	577	7	BQ086265	BQ086265 1j2p0e4_Y
C	602	194	21.4	1017	10	AB676542	BP335272	C	675	193.4	21.4	578	7	AQ615941	AQ615941 HS_5147_B
C	603	194	21.4	1017	7	AB676542	BP335272	C	676	193.4	21.4	579	7	AT132682	AT132682 nc75b05-x
C	604	194	21.4	1017	8	AB676542	BP335272	C	677	193.4	21.4	580	7	BK94125	BK94125 DKFP7797
C	605	194	21.4	1017	9	AB676542	BP335272	C	678	193.4	21.4	581	7	AQ887570	AQ887570 RCP111-14
C	606	194	21.4	1017	10	AB676542	BP335272	C	679	193.4	21.4	582	7	BK464282	BK464282 DKFP7781H
C	607	194	21.4	1017	11	AB676542	BP335272	C	680	193.4	21.4	583	7	BQ086265	BQ086265 1j2p0e4_Y
C	608	194	21.4	1017	12	AB676542	BP335272	C	681	193.4	21.4	584	7	CR542889	CR542889 DKFP459M
C	609	194	21.4	1017	13	AB676542	BP335272	C	682	193.4	21.4	585	7	CK822946	CK822946
C	610	194	21.4	1017	14	AB676542	BP335272	C	683	193					

C	682	193.4	21.3	2856	3	HSM803730	c	755	192.8	21.3	523	8	AZ517953
C	683	193.4	21.3	3505	3	CR749792	c	756	192.8	21.3	532	5	BW947715
C	684	193.2	21.3	321	5	BUT36659	c	757	192.8	21.3	570	1	AU145239
C	685	193.2	21.3	347	1	AB805546	c	758	192.8	21.3	584	8	AQ473656
C	686	193.2	21.3	377	5	BUR60886	c	759	192.8	21.3	599	1	A1363422
C	687	193.2	21.3	418	1	AA14618	c	760	192.8	21.3	605	8	AQ347764
C	688	193.2	21.3	453	1	AI44623	c	761	192.8	21.3	609	1	AV702857
C	689	193.2	21.3	482	2	BFR30052	c	762	192.8	21.3	612	7	CK905828
C	690	193.2	21.3	488	8	AW162555	c	763	192.8	21.3	617	8	B16477
C	691	193.2	21.3	498	8	AQ285474	c	764	192.8	21.3	636	5	BK83679
C	692	193.2	21.3	512	5	BX642479	c	765	192.8	21.3	651	9	AG057309
C	693	193.2	21.3	550	6	CD817781	c	766	192.8	21.3	658	7	CK430849
C	694	193.2	21.3	560	1	AL602775	c	767	192.8	21.3	659	8	AQ353815
C	695	193.2	21.3	577	1	AV732057	c	768	192.8	21.3	746	5	BW632972
C	696	193.2	21.3	579	2	AQ46539	c	769	192.8	21.3	1007	1	AU144110
C	697	193.2	21.3	589	2	AW162555	c	770	192.8	21.3	1176	3	CR612625
C	698	193.2	21.3	592	5	BQ272418	c	771	192.6	21.2	346	5	BW91496
C	699	193.2	21.3	604	8	AZ517781	c	772	192.6	21.2	370	5	BP250579
C	700	193.2	21.3	638	4	BG427437	c	773	192.6	21.2	420	1	AI049999
C	701	193.2	21.3	647	5	BX502809	c	774	192.6	21.2	519	8	AQ38500
C	702	193.2	21.3	658	7	BZ771947	c	780	192.6	21.2	655	9	AG080004
C	703	193.2	21.3	661	1	AV730440	c	781	192.6	21.2	656	9	AG052029
C	704	193.2	21.3	681	9	AG015022	c	776	192.6	21.2	659	8	AU144608
C	705	193.2	21.3	714	6	CD365358	c	777	192.6	21.2	682	7	BP2511408
C	706	193.2	21.3	767	1	AV700498	c	778	192.6	21.2	639	8	AQ18913
C	707	193.2	21.3	781	8	BZ771947	c	780	192.6	21.2	786	5	BP250579
C	708	193.2	21.3	799	1	BW632972	c	781	192.6	21.2	787	5	BP250579
C	709	193.2	21.3	888	5	BUL62525	c	782	192.6	21.2	788	5	BP250579
C	710	193.2	21.3	900	7	NA957335	c	783	192.6	21.2	789	5	BP250579
C	711	193.2	21.3	917	5	BUR63586	c	784	192.6	21.2	688	7	CA306131
C	712	193.2	21.3	919	3	BC012538	c	785	192.6	21.2	785	5	BUE29128
C	713	193	21.3	298	1	AR228979	c	786	192.6	21.2	698	6	CA306826
C	714	193	21.3	311	1	BU603673	c	787	192.6	21.2	716	5	BW9125
C	715	193	21.3	324	2	AW085626	c	788	192.6	21.2	718	2	AD039450
C	716	193	21.3	354	7	NS5456	c	789	192.6	21.2	756	5	BX341284
C	717	193	21.3	363	1	AA703393	c	790	192.6	21.2	803	6	CB962282
C	718	193	21.3	374	4	BI492613	c	791	192.6	21.2	901	5	BQ230657
C	719	193	21.3	375	2	AW021674	c	792	192.6	21.2	941	6	CD518779
C	720	193	21.3	382	1	AR568433	c	793	192.6	21.2	968	2	BP245228
C	721	193	21.3	388	8	AQ212798	c	794	192.6	21.2	1055	5	BP048298
C	722	193	21.3	413	8	AQ664885	c	795	192.6	21.2	1113	5	BW883957
C	723	193	21.3	433	2	AW157128	c	796	192.6	21.2	3180	3	BP245228
C	724	193	21.3	441	8	BW80074	c	797	192.6	21.2	3441	3	CR749847
C	725	193	21.3	456	2	AW897556	c	798	192.6	21.2	4667	3	BC038671
C	726	193	21.3	464	6	CR338317	c	799	192.6	21.2	291	2	AW42234
C	727	193	21.3	480	6	CD679321	c	800	192.4	21.2	302	4	BG296738
C	728	193	21.3	536	8	AQ393821	c	801	192.4	21.2	353	1	AA323290
C	729	193	21.3	541	1	AL600288	c	802	192.4	21.2	406	8	AS0227301
C	730	193	21.3	552	7	CN264709	c	803	192.4	21.2	366	1	AA1311605
C	731	193	21.3	553	2	BK848034	c	804	192.4	21.2	379	1	AI290008
C	732	193	21.3	561	8	AQ387133	c	805	192.4	21.2	387	6	CD708587
C	733	193	21.3	564	4	BI467196	c	806	192.4	21.2	393	8	ES177031
C	734	193	21.3	583	1	AL600288	c	807	192.4	21.2	402	8	BP047301
C	735	193	21.3	619	1	AG119007	c	808	192.4	21.2	406	8	BP17094
C	736	193	21.3	629	8	AQ73496	c	809	192.4	21.2	407	1	AA772906
C	737	193	21.3	642	8	BW59854	c	810	192.4	21.2	435	1	AI122175
C	738	193	21.3	648	8	BZ2611349	c	811	192.4	21.2	441	1	AI674873
C	739	193	21.3	663	4	BMT42716	c	812	192.4	21.2	447	8	AQ847172
C	740	193	21.3	681	7	BZ772377	c	813	192.4	21.2	452	1	BI383872
C	741	193	21.3	698	9	AG119007	c	814	192.4	21.2	477	7	CR738128
C	742	193	21.3	721	7	CR790056	c	815	192.4	21.2	483	2	BP013232
C	743	193	21.3	809	4	BK232499	c	816	192.4	21.2	490	5	BR138757
C	744	193	21.3	839	5	BK400315	c	817	192.4	21.2	498	5	BW959211
C	745	193	21.3	874	5	BW187815	c	818	192.4	21.2	504	8	BZ05467
C	746	193	21.3	890	3	CR59555	c	819	192.4	21.2	507	1	AA313025
C	747	193	21.3	2493	3	BC048794	c	820	192.4	21.2	518	4	BR738128
C	748	192.8	21.3	346	1	AA084148	c	821	192.4	21.2	545	8	AQ268517
C	749	192.8	21.3	371	2	CK00080	c	822	192.4	21.2	561	4	BI438652
C	750	192.8	21.3	425	2	AW513569	c	823	192.4	21.2	566	1	AL597545
C	751	192.8	21.3	430	2	AW513556	c	824	192.4	21.2	569	6	CA943760
C	752	192.8	21.3	493	8	BH1912810	c	825	192.4	21.2	570	1	AU149443
C	753	192.8	21.3	507	5	BQ787605	c	826	192.4	21.2	571	8	CK081323
C	754	192.8	21.3	512	2	AW473541	c	827	192.4	21.2	580	7	CK904663

C 828	829	192.4	21.2	585	1	A1571894	t202h06.x	901	192.2	21.2	716	9	AGI185392
B 829	830	192.4	21.2	606	5	BQ778458	1131d07.x	902	192.2	21.2	733	6	CR429975
C 830	831	192.4	21.2	607	5	BQ508704	DRKZP6686	903	192.2	21.2	734	6	CR45530
C 831	832	192.4	21.2	617	5	BQ632031	1121e05.x	904	192.2	21.2	751	7	CR490704
C 832	833	192.4	21.2	618	7	CN764754	170004244	905	192.2	21.2	775	8	BX351497
C 833	834	192.4	21.2	619	5	BK505458	DRKZP6686	906	192.2	21.2	783	8	AQ53777
C 834	835	192.4	21.2	621	5	BQ883717	AGENCCOURT	907	192.2	21.2	787	5	BW99347
C 835	836	192.4	21.2	621	7	CN277676	17000601	908	192.2	21.2	807	5	BW93347
C 836	837	192.4	21.2	632	5	BQ045015	UT-H-EDO-	909	192.2	21.2	904	5	BW168982
C 837	838	192.4	21.2	652	9	AG087320	Pan trogl	910	192.2	21.2	1034	5	BW188260
C 838	839	192.4	21.2	654	1	AU117926	AU117926	911	192.2	21.2	1034	3	CR611042
C 839	840	192.4	21.2	656	6	CA420015	UT-H-FHO-	912	192.2	21.2	1864	3	CR613224
C 840	841	192.4	21.2	665	7	CN243776	170004241	913	192.2	21.2	1884	3	CR594104
C 841	842	192.4	21.2	668	9	AG169531	Pan trogl	914	192.2	21.2	1886	3	CR625565
C 842	843	192.4	21.2	684	4	BG333118	602430809	915	192.2	21.2	1909	3	CR597717
C 843	844	192.4	21.2	709	6	CD237100	FNAGG09	916	192.2	21.2	1916	3	CR622212
C 844	845	192.4	21.2	712	6	CD246087	CD246087	917	192.2	21.2	2442	1	CR618116
C 845	846	192.4	21.2	721	6	CD564665	UT-H-FHT-	918	192.2	21.2	3049	1	AB847341
C 846	847	192.4	21.2	722	6	CN263776	170004241	919	192.2	21.2	343	1	AA636077
C 847	848	192.4	21.2	737	5	BK04515	DK2p686K	920	192.2	21.2	346	5	CD357102
C 848	849	192.4	21.2	745	9	AG085464	Pan trogl	921	192.2	21.2	353	5	BW937052
C 849	850	192.4	21.2	754	8	BK58486	BK58486	922	192.2	21.2	354	1	AT136687
C 850	851	192.4	21.2	778	6	CB985162	AGENCCOURT	923	192.2	21.2	355	2	AW771619
C 851	852	192.4	21.2	779	6	CR442904	UT-H-FDO-	924	192.2	21.2	490	1	AM182182
C 852	853	192.4	21.2	795	6	CF555558	AGENCCOURT	925	192.2	21.2	381	2	BR045167
C 853	854	192.4	21.2	885	6	CD514239	AGENCCOURT	926	192.2	21.2	447	8	CR434025
C 854	855	192.4	21.2	888	7	CR456538	AGENCCOURT	927	192.2	21.2	477	8	CD6341
C 855	856	192.4	21.2	1104	5	BK58486	BK58486	928	192.2	21.2	449	8	AK058688
C 856	857	192.4	21.2	1486	3	CR623651	CR623651	929	192.2	21.2	477	8	AQ198159
C 857	858	192.4	21.2	3540	3	CR442904	Homo sapi	930	192.2	21.2	490	1	CA43393
C 858	859	192.4	21.2	361	1	AA661583	nub6c08.B	931	192.2	21.2	381	2	BR045167
C 859	860	192.4	21.2	377	1	A152836	t21b06.x	932	192.2	21.2	477	8	CR434025
C 860	861	192.4	21.2	406	6	AQ213918	HS-2183.A	933	192.2	21.2	533	8	CD6341
C 861	862	192.4	21.2	418	1	AA917779	RBC-BT070	934	192.2	21.2	538	8	AK0417891
C 862	863	192.4	21.2	420	2	BE005811	RBC-BN012	935	192.2	21.2	542	6	CD661103
C 863	864	192.4	21.2	445	2	AA497824	tmb9910x	936	192.2	21.2	546	1	AB8847603
C 864	865	192.4	21.2	457	8	AQ224277	HS-2003_A	937	192.2	21.2	556	7	CR556759
C 865	866	192.4	21.2	468	5	BK101540	BK101540	938	192.2	21.2	556	4	BR944736
C 866	867	192.4	21.2	474	2	BB098911	RCB-BT070	939	192.2	21.2	553	1	AT171338
C 867	868	192.4	21.2	483	1	AA917779	oq947b12.8	940	192.2	21.2	538	8	AK0417891
C 868	869	192.4	21.2	484	8	AQ535388	RPC11-1.3	941	192.2	21.2	542	6	CD661103
C 869	870	192.4	21.2	493	2	BE551574	601076903	942	192.2	21.2	558	4	BG8337603
C 870	871	192.4	21.2	499	8	AQ539985	RPC11-11-3	943	192.2	21.2	614	2	AM151824
C 871	872	192.4	21.2	517	8	AQ36199	RPC11-13	944	192.2	21.2	555	1	AV719906
C 872	873	192.4	21.2	518	1	AA157319	AE177199	945	192.2	21.2	554	1	AT171338
C 873	874	192.4	21.2	526	6	AA493937	UT-H-DIO-	946	192.2	21.2	568	2	BE144554
C 874	875	192.4	21.2	534	5	BK52385	DKEF9779M	947	192.2	21.2	801	4	BG537968
C 875	876	192.4	21.2	564	8	AQ006337	CIT-HSP-2	948	192.2	21.2	623	8	AM991111
C 876	877	192.4	21.2	569	4	BM263248	1972c10.x	949	192.2	21.2	614	2	AM151824
C 877	878	192.4	21.2	577	8	BM333667	1950d12.x	950	192.2	21.2	620	1	AV719906
C 878	879	192.4	21.2	584	5	AQ483308	RPC11-11-2	951	192.2	21.2	620	1	AV719906
C 879	880	192.4	21.2	589	6	CB052611	NISC_qm08	952	192.2	21.2	621	8	AK035723
C 880	881	192.4	21.2	591	2	BE276666	601147484	953	192.2	21.2	622	8	AD550760
C 881	882	192.4	21.2	594	4	BM770671	K-BE270012	954	192.2	21.2	623	8	AM991111
C 882	883	192.4	21.2	605	6	CA423390	RPC11-11-2	955	192.2	21.2	624	1	AV719906
C 883	884	192.4	21.2	609	8	AQ540554	RPC11-11-3	956	192.2	21.2	625	1	AV719906
C 884	885	192.4	21.2	612	7	CKB18280	1C2F12.Y	957	192.2	21.2	626	1	AV719906
C 885	886	192.4	21.2	629	7	CN360036	170005313	958	192.2	21.2	627	1	AT0543
C 886	887	192.4	21.2	630	2	AW957739	BS176989	959	192.2	21.2	801	4	BC032901
C 887	888	192.4	21.2	630	8	AQ266645	RPC11-14	960	192.2	21.2	874	1	AT0543
C 888	889	192.4	21.2	636	8	AQ266645	RPC11-74	961	192.2	21.2	894	5	BCX33934
C 889	890	192.4	21.2	650	5	BK623224	DKEF9779M	962	192.2	21.2	698	9	AGJ166699
C 890	891	192.4	21.2	683	5	BK184851	AGENCCOURT	963	192.2	21.2	700	1	AT0543
C 891	892	192.4	21.2	692	7	BM97147	UT-H-FGI	964	192.2	21.2	701	1	AT0543
C 892	893	192.4	21.2	699	9	AG105245	Pan trogl	965	192.2	21.2	702	1	AT0543
C 893	894	192.4	21.2	700	8	AQ375664	RPC11-14	966	192.2	21.2	703	1	AT0543
C 894	895	192.4	21.2	701	6	CA439730	UT-H-DIO-	967	192.2	21.2	704	1	AT0543
C 895	896	192.4	21.2	702	4	BK184851	AGENCCOURT	968	192.2	21.2	705	1	AT0543
C 896	897	192.4	21.2	708	7	BQ183748	UT-H-EUO-	969	192.2	21.2	706	1	AT0543
C 897	898	192.4	21.2	711	5	BKU262395	UT-H-FGI	970	192.2	21.2	707	1	AT0543
C 898	899	192.4	21.2	714	7	CN409711	UT-H-FGI	971	192.2	21.2	708	1	AT0543
C 899	900	192.4	21.2	715	2	BE742024	UT-H-FGI	972	192.2	21.2	709	1	AT0543

C 974	191.8	21.1	573	5	BW992855	BM92855 UI-H-DTO-	c1047	191.4	21.1	445	1	AA426451
C 975	191.8	21.1	609	5	BQ542460	BQ49460 1107c12.x	c1048	191.4	21.1	456	7	CR446133
C 976	191.8	21.1	614	5	BX952334	BX952334 DRPDT10	c1049	191.4	21.1	450	1	CR446133
C 977	191.8	21.1	638	8	AQ32583	AQ32583 RPC11-93	c1050	191.4	21.1	469	5	RC1-H-TD0-
C 978	191.8	21.1	644	9	AG039567	AG038567 Pan trogl	c1051	191.4	21.1	470	1	BQ029488
C 979	191.8	21.1	671	1	AV648659	AV648659 AV648659	c1052	191.4	21.1	492	8	AQ480120
C 980	191.8	21.1	678	8	AQ553340	AQ553340 RPC1-11-4	c1053	191.4	21.1	493	4	BM509931
C 981	191.8	21.1	686	9	AG001462	AG001462 Homo sapi	c1054	191.4	21.1	504	4	BM64427
C 982	191.8	21.1	693	9	AG001472	AG001472 Homo sapi	c1055	191.4	21.1	505	8	AO052041
C 983	191.8	21.1	695	8	AQ546366	AQ546366 CITBI-EI-	c1056	191.4	21.1	514	8	AQ002001
C 984	191.8	21.1	714	1	AV700858	AV700858 AV700858	c1057	191.4	21.1	555	8	BH2781 RPC11-17M1
C 985	191.8	21.1	735	2	BFR81427	BFR81427 602155631	c1058	191.4	21.1	556	8	AQ372425
C 986	191.8	21.1	750	5	BX509484	BX509484 DKKF266861	c1059	191.4	21.1	570	5	BX509484
C 987	191.8	21.1	759	8	BZ2610496	BZ2610496 WHAD11GTP	c1060	191.4	21.1	577	5	BP152045
C 988	191.8	21.1	836	2	BC034527	BC034527 Homo sapi	c1061	191.4	21.1	580	5	BM638992
C 989	191.8	21.1	873	6	CA454910	CA454910 AGENCOURT	c1062	191.4	21.1	581	5	BK096770
C 990	191.8	21.1	882	2	BFR81427	BFR81427 602155631	c1063	191.4	21.1	585	8	BH2781 RPC11-17M1
C 991	191.8	21.1	884	2	CFR47402	CFR47402 602181853	c1064	191.4	21.1	619	1	AG118439
C 992	191.8	21.1	911	5	BQ719276	BQ719276 AGENCOURT	c1065	191.4	21.1	638	6	CB151593
C 993	191.8	21.1	1057	4	BG758151	BG758151 602712320	c1066	191.4	21.1	639	5	BM92802
C 994	191.8	21.1	1077	4	BW30297	BW30297 AGENCOURT	c1067	191.4	21.1	655	6	CA147141
C 995	191.8	21.1	1146	4	BMS63064	BMS63064 AGENCOURT	c1068	191.4	21.1	656	9	AG058334
C 996	191.8	21.1	1226	3	BC033679	BC033679 Homo sapi	c1069	191.4	21.1	679	1	BQ777329
C 997	191.8	21.1	2213	3	CRB23485	CRB23485 full-leng	c1070	191.4	21.1	684	1	AV731385
C 998	191.8	21.1	311	5	BUR930045	BUR930045 AGENCOURT	c1071	191.4	21.1	693	1	CB151593
C 999	191.8	21.1	329	7	TII0218	TII0218 Seq919 b4HB	c1072	191.4	21.1	729	5	BP231303
C 1000	191.8	21.1	334	2	BF447461	BF447461 nae37df5	c1073	191.4	21.1	736	7	CN278157
C 1001	191.8	21.1	350	7	T03576	T03576 IB501 Infan	c1074	191.4	21.1	745	2	BE882869
C 1002	191.8	21.1	379	1	BFT39035	BFT39035 PM4-KT004	c1075	191.4	21.1	747	1	CB385823
C 1003	191.8	21.1	404	1	A133433	A133433 qo70112.x	c1076	191.4	21.1	764	9	CI423322 RP11-29A7
C 1004	191.8	21.1	430	2	BF940837	BF940837 7d99f09.x	c1077	191.4	21.1	770	4	BG7070708
C 1005	191.8	21.1	451	1	AV706458	AV706458 AV706458	c1078	191.4	21.1	779	5	BP231303
C 1006	191.8	21.1	472	1	AU150222	AU150222 AU150222	c1079	191.4	21.1	785	4	BM503933
C 1007	191.8	21.1	479	1	AO565262	AO565262 HS 5355_B	c1080	191.4	21.1	793	4	BP680709
C 1008	191.8	21.1	494	1	A133433	A133433 qt78e11.x	c1081	191.4	21.1	795	2	BR882032
C 1009	191.8	21.1	500	9	AG029034	AG029034 Homo sapi	c1082	191.4	21.1	797	1	BUS944090
C 1010	191.8	21.1	505	8	AZ254926	AZ254926 UP 341-6L	c1083	191.4	21.1	809	5	BP272915
C 1011	191.8	21.1	510	5	BK482171	BK482171 DRF266861	c1084	191.4	21.1	815	4	BM55132
C 1012	191.8	21.1	518	5	BW83911	BW83911 UT-CP-ENP	c1085	191.4	21.1	834	3	CR623688
C 1013	191.8	21.1	524	8	AO565262	AO565262 HS 5355_B	c1086	191.4	21.1	845	2	AY203942
C 1014	191.8	21.1	532	4	BW309845	BW309845 iho8812.y	c1087	191.4	21.1	858	1	CR625869
C 1015	191.8	21.1	566	2	AW968338	AW968338 EST880413	c1088	191.4	21.1	878	3	CR20860
C 1016	191.8	21.1	573	2	AW162314	AW162314 au66d06.x	c1089	191.4	21.1	879	8	BC033247
C 1017	191.8	21.1	582	7	CK825971	CK825971 1k36112.x	c1090	191.4	21.1	880	3	BM55132 AGENCOURT
C 1018	191.8	21.1	613	9	AO00717	AO00717 CIRTHSP-2	c1091	191.4	21.1	881	3	CR623688
C 1019	191.8	21.1	640	9	AG058581	AG058581 Pan trogl	c1092	191.4	21.1	888	3	AY203942 Homo sapi
C 1020	191.8	21.1	649	9	AG066959	AG066959 Pan trogl	c1093	191.4	21.1	899	1	CR42024
C 1021	191.8	21.1	656	1	AL05672	AL05672 DKF26686A	c1094	191.4	21.1	900	1	AM195822 RP11-29A7
C 1022	191.8	21.1	674	8	AQ470397	AQ470397 CITBI-EI-	c1095	191.4	21.1	909	1	BC033247
C 1023	191.8	21.1	678	2	AW162332	AW162332 au74b03.x	c1096	191.4	21.1	916	1	BM55132
C 1024	191.8	21.1	678	9	AG162202	AG162202 Pan trogl	c1097	191.4	21.1	917	1	AY703785
C 1025	191.8	21.1	679	2	BTP46320	BTP46320 602018525	c1098	191.4	21.1	918	1	AV03785
C 1026	191.8	21.1	680	5	BX507811	BX507811 DKF26686A	c1099	191.4	21.1	919	1	BP530611
C 1027	191.8	21.1	702	9	AG164596	AG164596 Pan trogl	c1100	191.4	21.1	920	1	BP680809
C 1028	191.8	21.1	831	2	CR608042	CR608042 602134084	c1101	191.4	21.1	921	1	CM42004
C 1029	191.8	21.1	856	8	AQ891549	AQ891549 HS 3143_A	c1102	191.4	21.1	922	1	AM053673
C 1030	191.8	21.1	891	5	BX383723	BX383723 BX383723	c1103	191.4	21.1	923	1	AT1590442
C 1031	191.8	21.1	924	5	BUB857128	BUB857128 AGENCOURT	c1104	191.4	21.1	924	1	AV703785
C 1032	191.8	21.1	945	5	BUS27626	BUS27626 AGENCOURT	c1105	191.4	21.1	925	1	BP530611
C 1033	191.8	21.1	1250	3	BC016813	BC016813 Homo Bapi	c1106	191.4	21.1	926	1	AO093841 HS 3103_B
C 1034	191.8	21.1	1255	3	CR608042	CR608042 full-leng	c1107	191.4	21.1	927	1	AQ114248 CIT-HSP-2
C 1035	191.8	21.1	340	8	AQ230483	AQ230483 HS 2041_B	c1108	191.4	21.1	928	1	AQ057953 CIT-HSP-2
C 1036	191.8	21.1	343	1	AA338474	AA338474 EST88451	c1109	191.4	21.1	929	1	BQ955970 AGENCOURT
C 1037	191.8	21.1	345	2	AW731858	AW731858 ba02a04.x	c1110	191.4	21.1	930	1	AQ226590 HS 2010_A
C 1038	191.8	21.1	384	1	AW572299	AW572299 UI-HR-BNO	c1111	191.4	21.1	931	1	CM275115
C 1039	191.8	21.1	389	1	AR807704	AR807704 nw3106_g	c1112	191.4	21.1	932	1	CM275115
C 1040	191.8	21.1	407	1	AA653513	AA653513 ag66106_s	c1113	191.4	21.1	933	1	AQ236686 RPC11-6
C 1041	191.8	21.1	416	21.1	AQ132995	AQ132995 wo55b07_x	c1114	191.4	21.1	934	1	AQ412029 RPC11-1
C 1042	191.8	21.1	432	8	AQ351800	AQ351800 CITBI-EI-	c1115	191.4	21.1	935	1	BI077884 im94e07_x
C 1043	191.8	21.1	434	5	BQ181725	BQ181725 UT-HR-EUO-	c1116	191.4	21.1	936	1	BP88821 AGENCOURT
C 1044	191.8	21.1	435	7	CN256570	CN256570 17000600	c1117	191.4	21.1	937	1	AQ487852 RPC11-2
C 1045	191.8	21.1	437	1	A1038029	A1038029 ox29f12.x	c1118	191.4	21.1	938	1	BU17885 AGENCOURT
C 1046	191.8	21.1	437	1	A1046	A1046	c1119	191.2	21.1	939	1	AQ625967 RPC11-14

c1120	191.2	21.1	678	6	CN422648	UI-H-FLO-	c1193	190.8	21.0	583	4	B1467327	ic22h11.x
c1121	191.2	21.1	694	4	BM686366	UI-E-CRO-	c1194	190.8	21.0	584	5	BU078874	1m71d06.x
c1122	191.2	21.1	705	1	AV73420		c1195	190.8	21.0	624	2	BP218253	
c1123	191.2	21.1	729	1	AV70541		c1196	190.8	21.0	648	5	BQ894783	AGENCOURT
c1124	191.2	21.1	779	8	AQ63096	RPC1-11-4	c1197	190.8	21.0	657	5	BUD26531	UI-H-PTO-
c1125	191.2	21.1	851	2	BF346854		c1198	190.8	21.0	658	9	AG183592	Pan trogl
c1126	191.2	21.1	1073	8	BZ601227	WHADC89TR	c1199	190.8	21.0	665	8	A2520516	A2520516 RPC1-11-3
c1127	191.2	21.1	1074	3	CR620015	full-leng	c1200	190.8	21.0	667	8	B2602960	WHADC156TR
c1128	191.2	21.1	3035	3	HSM80842		c1201	190.8	21.0	670	9	AG051703	
c1129	191.2	21.1	4274	16	HSMW04027		c1202	190.8	21.0	677	8	AQ487101	
c1130	191.2	21.1	4274	8	CR43398		c1203	190.8	21.0	679	9	AG114427	Pan trogl
c1131	191.2	21.1	381	5	BX641388		c1204	190.8	21.0	680	9	AG176489	Pan trogl
c1132	191.2	21.1	454	1	AA431911		c1205	190.8	21.0	682	5	BM994908	
c1133	191.2	21.1	402	8	CK906008		c1206	190.8	21.0	709	1	AV649109	
c1134	191.2	21.1	406	5	BUS00507		c1207	190.8	21.0	714	9	AQ878839	HS 3144 B
c1135	191.2	21.1	418	7	CR773797		c1208	190.8	21.0	716	5	BUE17628	
c1136	191.2	21.1	423	8	AQ418173		c1209	190.8	21.0	720	4	BG701628	
c1137	191.2	21.1	453	1	AA157876		c1210	190.8	21.0	727	5	BMM90571	
c1138	191.2	21.1	454	7	AA1340151		c1211	190.8	21.0	727	6	CA442999	
c1139	191.2	21.1	481	7	CK906008		c1212	190.8	21.0	737	2	BE904397	
c1140	191.2	21.1	498	6	CA434081		c1213	190.8	21.0	737	6	CA417973	
c1141	191.2	21.1	504	8	BUR49552	UI-H-BNO	c1214	190.8	21.0	748	1	A1017573	
c1142	191.2	21.1	524	8	AQ355203	CITB1-B1-	c1215	190.8	21.0	774	6	CD35237	
c1143	191.2	21.1	535	1	AA046906	zr47601.r	c1216	190.8	21.0	904	5	BQ70416	AGENCOURT
c1144	191.2	21.1	535	1	AT760850		c1217	190.8	21.0	913	5	BX390441	
c1145	191.2	21.1	544	8	AQ678189		c1218	190.8	21.0	932	4	BG338510	
c1146	191.2	21.1	550	8	AQ393346		c1219	190.8	21.0	1023	1	AL523272	
c1147	191.2	21.1	551	8	AQ42689	CITB1-E1-	c1220	190.8	21.0	1145	4	BM64744	AGENCOURT
c1148	191.2	21.1	557	4	BR091156	192807.Y	c1221	190.8	21.0	1471	3	CR612064	
c1149	191.2	21.1	557	5	BX470626	DKF2p68J	c1222	190.8	21.0	1542	1	CR61917	full-leng
c1150	191.2	21.1	566	1	AU147463	AU147463	c1223	190.8	21.0	1619	3	HSMB4364	
c1151	191.2	21.1	574	2	AW975139	EST37245	c1224	190.8	21.0	1659	3	CR602249	
c1152	191.2	21.1	576	5	BUR66665	UI-CF-DU1	c1225	190.8	21.0	2504	8	CR621797	
c1153	191.2	21.1	579	8	AR970950	EST38033	c1226	190.8	21.0	2782	3	BB05805	
c1154	191.2	21.1	586	8	AC320497		c1227	190.8	21.0	3127	3	AF447879	
c1155	191.2	21.1	613	5	BQ267948	1J96971.X	c1228	190.8	21.0	330	5	BUE66680	
c1156	191.2	21.1	619	5	BX485408	DKF2p68B	c1229	190.8	21.0	335	2	AW117860	
c1157	191.2	21.1	627	8	AR022911	RPC11-65	c1230	190.8	21.0	381	2	AW273389	
c1158	191.2	21.1	630	6	CA428075	UI-H-DE0-	c1231	190.8	21.0	420	8	AQ371087	
c1159	191.2	21.1	646	4	BX533669	6031935989	c1232	190.8	21.0	420	8	BB9781	CTT-HSP-217
c1160	191.2	21.1	697	9	AG01078	Homo sapi	c1233	190.8	21.0	422	2	BB089817	RC5-BTO70
c1161	191.2	21.1	700	4	BX259846	602971503	c1234	190.8	21.0	432	2	BW627747	
c1162	191.2	21.1	730	4	BX402367	BX402367	c1235	190.8	21.0	438	7	CR739570	
c1163	191.2	21.1	767	5	BQ775984	UI-H-FM0-	c1236	190.8	21.0	438	7	BZ99910	WHAC195TR
c1164	191.2	21.1	788	4	BA497601	601859491	c1237	190.8	21.0	444	8	AO71087	HS 3139 A
c1165	191.2	21.1	895	4	AQ74667	HS 2273 A	c1238	190.8	21.0	444	8	BB05805	RC2-BN012
c1166	191.2	21.1	914	6	CD517002	AGENCOURT	c1239	190.8	21.0	461	1	BW627747	hh9103.x
c1167	191.2	21.1	951	5	BQ276534	AGENCOURT	c1240	190.8	21.0	472	1	AA572983	nm33d11.B
c1168	191.2	21.1	965	5	BX227005	AGENCOURT	c1241	190.8	21.0	476	7	N67313	Y*51e02_81
c1169	191.2	21.1	994	5	BX400912	BX400912	c1242	190.8	21.0	486	7	BX496224	DKF2p77N
c1170	191.2	21.1	1044	5	BW507799	AGENCOURT	c1243	190.8	21.0	486	7	CN276954	17006001
c1171	191.2	21.1	1063	1	AL517454	AL517454	c1244	190.8	21.0	487	5	BX954464	DKF2p781N
c1172	191.2	21.1	1087	6	CD01398	90138017	c1245	190.8	21.0	497	5	BUE663299	g19812.z
c1173	191.2	21.1	2798	3	BC038117	Homo Sapi	c1246	190.8	21.0	523	2	BRP50372	nab2293.
c1174	191.2	21.1	3016	5	BC068461	Romo Sapi	c1247	190.8	21.0	527	2	BB877331	601495564
c1175	191.2	21.1	298	2	AW150899	XG53f03.x	c1248	190.8	21.0	544	8	AQ506882	RPC11-3
c1176	191.2	21.1	344	1	BAE138387	X774C03.x	c1249	190.8	21.0	552	1	A1921706	w02908.x
c1177	191.2	21.1	477	1	AD702171	ff87e11.b	c1250	190.8	21.0	561	5	BX504341	DKF2p68K
c1178	191.2	21.1	402	1	AV695953	AV695953	c1251	190.8	21.0	561	5	AQ484348	RPC11-11
c1179	191.2	21.1	406	7	N42298	Y~22910..91	c1252	190.8	21.0	571	1	AQ313925	RPC11-10
c1180	191.2	21.1	418	1	AI434103	t:131b05.x	c1253	190.8	21.0	579	8	BB877331	601495564
c1181	191.2	21.1	437	7	CN277621	17006001	c1254	190.8	21.0	606	8	BX48342	DKF2p686D
c1182	191.2	21.1	448	1	AA632355	mp1e15.b	c1255	190.8	21.0	629	5	BX507857	DKF2p686D
c1183	191.2	21.1	477	1	AT1733647	an220h08.x	c1256	190.8	21.0	638	6	CB055260	NIS_C gm08
c1184	191.2	21.1	402	1	CD516047	AGENCOIRT	c1257	190.8	21.0	644	7	CV368474	PM2-DT004
c1185	191.2	21.1	494	1	AT733662	an228907.x	c1258	190.8	21.0	651	6	CA778069	ip17e11.x
c1186	191.2	21.1	500	6	CD432771	UT-H-DE0-	c1259	190.8	21.0	659	2	AQ322876	RPC11-11
c1187	191.2	21.1	516	8	AQ828909	RFC1-11-2	c1260	190.8	21.0	669	9	AG123283	Pan trogl
c1188	191.2	21.1	517	1	A1003086	an24d09.b	c1261	190.8	21.0	674	9	AG123283	Pan trogl
c1189	191.2	21.1	517	1	AU157945	AU157945	c1262	190.8	21.0	677	6	CR397305	c893..Y
c1190	191.2	21.1	544	4	BM091382	ic22a08.x	c1263	190.8	21.0	680	5	BQ773564	UI-H-FB0-
c1191	191.2	21.1	574	4	BM787339	K-EST066	c1264	190.8	21.0	693	8	AQ445780	RPC11-11-1
c1192	191.2	21.1	576	6	CA427630		c1265	190.8	21.0	711	6	CR445780	

c1266	190.6	21.0	723	6	CA431699	1339	190.2	21.0	469	5	BUE60220
c1267	190.6	21.0	727	5	BUS61234	c1340	190.2	21.0	470	8	AQ226326
c1268	190.6	21.0	753	1	AL691630	c1341	190.2	21.0	477	2	AQ32842
c1269	190.5	21.0	801	5	BQ214885	c1342	190.2	21.0	490	8	AQ432147
c1270	190.6	21.0	833	4	BG286471	c1343	190.2	21.0	494	2	BB080768
c1271	190.6	21.0	882	1	BQ288201	c1344	190.2	21.0	498	1	CR88711
c1272	190.6	21.0	890	4	BG163987	c1345	190.2	21.0	520	6	CA946754
c1273	190.6	21.0	895	2	BP674823	c1346	190.2	21.0	525	8	AQ082123
c1274	190.6	21.0	949	1	AL568770	c1347	190.2	21.0	528	8	B5595
c1275	190.6	21.0	1065	4	BW454948	c1348	190.2	21.0	552	4	B123275
c1276	190.6	21.0	1088	4	BW477840	c1349	190.2	21.0	564	5	BUR60291
c1277	190.6	21.0	1088	3	HSM80883	c1350	190.2	21.0	566	5	B1957747
c1278	190.6	21.0	8421	3	HSM80381	c1351	190.2	21.0	570	8	AQ018599
c1279	190.4	21.0	398	1	AB857377	c1352	190.2	21.0	574	8	AQ507060
c1280	190.4	21.0	454	4	BG006718	c1353	190.2	21.0	577	8	AA14093
c1281	190.4	21.0	481	1	AL707639	c1354	190.2	21.0	589	8	AQ041600
c1282	190.4	21.0	492	1	AA167556	c1355	190.2	21.0	601	5	BX5080291
c1283	190.4	21.0	498	1	AA1747481	c1356	190.2	21.0	607	8	B1663705
c1284	190.4	21.0	453	1	AT744830	c1357	190.2	21.0	607	9	AG018337
c1285	190.4	21.0	454	4	BP674823	c1358	190.2	21.0	613	7	W27084
c1286	190.4	21.0	454	4	AL707639	c1359	190.2	21.0	625	9	AG018336
c1287	190.4	21.0	487	1	AA161831	c1360	190.2	21.0	637	8	AQ423458
c1288	190.4	21.0	487	8	AQ425255	c1361	190.2	21.0	639	1	CA080170
c1289	190.4	21.0	492	8	AQ198722	c1362	190.2	21.0	663	1	CA080170
c1290	190.4	21.0	494	8	AQ32572	c1363	190.2	21.0	666	9	AG040280
c1291	190.4	21.0	502	8	AQ391359	c1364	190.2	21.0	666	9	AG182057
c1292	190.4	21.0	524	9	BU786222	c1365	190.2	21.0	667	9	AG165154
c1293	190.4	21.0	552	8	AQ377725	c1366	190.2	21.0	672	1	AV648612
c1294	190.4	21.0	556	8	AQ800806	c1367	190.2	21.0	687	1	AI74827
c1295	190.4	21.0	569	8	AZ520604	c1368	190.2	21.0	695	9	AG178603
c1296	190.4	21.0	582	5	BP336447	c1369	190.2	21.0	699	7	CR709789
c1297	190.4	21.0	623	5	BU072384	c1370	190.2	21.0	705	9	AG113042
c1298	190.4	21.0	629	5	BT786222	c1371	190.2	21.0	709	9	AG0632003
c1299	190.4	21.0	655	9	AG134408	c1372	190.2	21.0	709	9	AG143216
c1300	190.4	21.0	657	9	AQ624700	c1373	190.2	21.0	721	3	BC017436
c1301	190.4	21.0	664	9	AG056105	c1374	190.2	21.0	728	8	AG085756
c1302	190.4	21.0	667	9	AG159164	c1375	190.2	21.0	731	4	AG156069
c1303	190.4	21.0	668	9	AG146787	c1376	190.2	21.0	738	8	AG113042
c1304	190.4	21.0	679	9	AG159116	c1377	190.2	21.0	749	1	AL572160
c1305	190.4	21.0	676	9	AG164176	c1378	190.2	21.0	750	5	BQ213854
c1306	190.4	21.0	731	4	BM662995	c1379	190.2	21.0	751	3	BC017436
c1307	190.4	21.0	732	4	CA422125	c1380	190.2	21.0	752	3	BC017436
c1308	190.4	21.0	741	7	CR748203	c1381	190.2	21.0	753	8	AG159164
c1309	190.4	21.0	759	5	BQ014487	c1382	190.2	21.0	758	9	AG146787
c1310	190.4	21.0	769	5	BQ710315	c1383	190.2	21.0	759	9	AG159116
c1311	190.4	21.0	776	9	CB308284	c1384	190.2	21.0	760	1	AI735609
c1312	190.4	21.0	829	6	CB308284	c1385	190.2	21.0	761	4	BG112362
c1313	190.4	21.0	861	8	AQ897084	c1386	190.2	21.0	762	1	BC017436
c1314	190.4	21.0	877	5	BQ953835	c1387	190.2	21.0	763	1	BC017436
c1315	190.4	21.0	911	6	CD520000	c1388	190.2	21.0	768	3	BC037785
c1316	190.4	21.0	938	9	CL423157	c1389	190.2	21.0	769	8	AQ278103
c1317	190.4	21.0	947	5	BQ707946	c1390	190.2	21.0	770	9	AG192205
c1318	190.4	21.0	954	2	BE61927	c1391	190.2	21.0	771	9	AG164176
c1319	190.4	21.0	987	5	BK417024	c1392	190.2	21.0	772	1	BC017436
c1320	190.4	21.0	1007	1	AL548332	c1393	190.2	21.0	773	1	BC017436
c1321	190.4	21.0	1122	1	AL525584	c1394	190.2	21.0	774	1	BC017436
c1322	190.4	21.0	1306	3	BC022398	c1395	190.2	21.0	775	1	BC017436
c1323	190.4	21.0	364	1	CR742655	c1396	190.2	21.0	776	1	BC017436
c1324	190.4	21.0	4086	3	HSM807683	c1397	190.2	21.0	777	1	BC017436
c1325	190.4	21.0	4717	5	BC03267	c1398	190.2	21.0	778	1	BC017436
c1326	190.4	21.0	7180	3	HSM804869	c1399	190.2	21.0	779	1	BC017436
c1327	190.4	21.0	7318	7	N55076	c1400	190.2	21.0	780	1	BC017436
c1328	190.4	21.0	7405	1	AR510108	c1401	190.2	21.0	781	1	BC017436
c1329	190.4	21.0	7556	1	AR343923	c1402	190.2	21.0	782	1	BC017436
c1330	190.4	21.0	7694	1	AA084320	c1403	190.2	21.0	783	1	BC017436
c1331	190.4	21.0	7891	1	AA158106	c1404	190.2	21.0	784	1	BC017436
c1332	190.4	21.0	8081	1	AA1362442	c1405	190.2	21.0	785	1	BC017436
c1333	190.4	21.0	8261	1	AA1362442	c1406	190.2	21.0	786	1	BC017436
c1334	190.4	21.0	8344	1	AA1703108	c1407	190.2	21.0	787	1	BC017436
c1335	190.4	21.0	8356	1	AA1703108	c1408	190.2	21.0	788	1	BC017436
c1336	190.4	21.0	8364	1	AA1703108	c1409	190.2	21.0	789	1	BC017436
c1337	190.4	21.0	8399	1	AA1703108	c1410	190.2	21.0	790	1	BC017436
c1338	190.4	21.0	8408	1	AA1703108	c1411	190.2	21.0	791	1	BC017436
1	AA1703108	c1412	190.2	21.0	792	1	BC017436	c1413	190.2	21.0	793
2	AA1703108	c1414	190.2	21.0	794	1	BC017436	c1415	190.2	21.0	795
3	AA1703108	c1416	190.2	21.0	796	1	BC017436	c1417	190.2	21.0	797
4	AA1703108	c1418	190.2	21.0	798	1	BC017436	c1419	190.2	21.0	799
5	AA1703108	c1420	190.2	21.0	799	1	BC017436	c1421	190.2	21.0	800
6	AA1703108	c1422	190.2	21.0	800	1	BC017436	c1423	190.2	21.0	801
7	AA1703108	c1424	190.2	21.0	801	1	BC017436	c1425	190.2	21.0	802
8	AA1703108	c1426	190.2	21.0	802	1	BC017436	c1427	190.2	21.0	803
9	AA1703108	c1428	190.2	21.0	803	1	BC017436	c1429	190.2	21.0	804
10	AA1703108	c1430	190.2	21.0	804	1	BC017436	c1431	190.2	21.0	805
11	AA1703108	c1432	190.2	21.0	805	1	BC017436	c1433	190.2	21.0	806
12	AA1703108	c1434	190.2	21.0	806	1	BC017436	c1435	190.2	21.0	807
13	AA1703108	c1436	190.2	21.0	807	1	BC017436	c1437	190.2	21.0	808
14	AA1703108	c1438	190.2	21.0	808	1	BC017436	c1439	190.2	21.0	809
15	AA1703108	c1440	190.2	21.0	809	1	BC017436	c1441	190.2	21.0	810
16	AA1703108	c1442	190.2	21.0	810	1	BC017436	c1443	190.2	21.0	811
17	AA1703108	c1444	190.2	21.0	811	1	BC017436	c1445	190.2	21.0	812
18	AA1703108	c1446	190.2	21.0	812	1	BC017436	c1447	190.2	21.0	813
19	AA1703108	c1448	190.2	21.0	813	1	BC017436	c1449	190.2	21.0	814
20	AA1703108	c1450	190.2	21.0	814	1	BC017436	c1451	190.2	21.0	815
21	AA1703108	c1452	190.2	21.0	815	1	BC017436	c1453	190.2	21.0	816
22	AA1703108	c1454	190.2	21.0	816	1	BC017436	c1455	190.2	21.0	817
23	AA1703108	c1456	190.2	21.0	817	1	BC017436	c1457	190.2	21.0	818
24	AA1703108	c1458	190.2	21.0	818	1	BC017436	c1459	190.2	21.0	819
25</											

FEATURES	B source	Location/Qualifiers
		1. - .650
/organism="Homo sapiens"		
/mol_type="mRNA"		
/db_xref="taxon:9606"		
/clone="UI-H-DFO-024-0-UT"		
/tissue_type="Subchondral Bone"		
/dev_stage="Adult"		
/lab_hosca="DHIOB (Life Technologies)"		
/clone_lib="NCI CGAP DFO"		
/note="Organ: Bone; Vector: pTT7-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP DFO is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Leinon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7- <i>lacZ</i> . The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dr)18 tail. The		

		TITLE	Shotgun sequencing of the human transcriptome with ORF expressed
		JOURNAL	Sequence tags
		MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
		PUBMED	2022663
ORIGIN		COMMENT	10737800
Query	Match	Best Local Similarity	67.9%; Score 616.2; DB 6; Length 650;
		Conservative	99.4%; Pred. No. 7.4e-91;
		Mismatches	0; Indels 3; Gaps 1;
Db	650	PIGCCACACAGAGACTGGCGCCAGGAGAACAGTCTCTGTGCTTGAA	TTGGA 335
Qy	276	AGTCCACACAGAGACTGGCGCCAGGAGAACAGTCTCTGTGCTTGAA	TTGGA 591
Db	650	AGTCCACACAGAGACTGGCGCCAGGAGAACAGTCTCTGTGCTTGAA	TTGGA 591
Qy	336	CAGTAGAGGAGTCCTGACCACTCC-AGGGGGGGGGGAACTCTCATTA	AGGAGGAGA 394
Db	590	CAGTAGAGGAGTCCTGACCACTCC-AGGGGGGGGGGAACTCTCATTA	AGGAGGAGA 531
Qy	395	GGCTCTGGCCCCCACAGACTCTGCCTCTGCTCTGCTCTGCGCAGTGG	GAG 454
Db	530	GGCTCTGGCCCCCACAGACTCTGCCTCTGCTCTGCTCTGCGCAGTGG	GAG 471
Qy	455	TGGCACAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GGGG 514
Db	470	TGGCACAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GGGG 411
Qy	515	GTCCCTGCTTGGCGCACTCTGCTCTGCTCTGCTCTGCTCTGCTCTG	CTG 574
Db	410	GTCCCTGCTTGGCGCACTCTGCTCTGCTCTGCTCTGCTCTGCTCTG	CTG 351
Qy	575	TGTATCTATGATTACACATTAGCAATAAACACACAGGCTGATTTG	GGGAGGT 634
Db	350	TGTATCTATGATTACACATTAGCAATAAACACACAGGCTGATTTG	GGGAGGT 291
Qy	635	GGCTCAAGCTGTAATCCAGCACTTGGGGCGAGGGGGGGGGGGGG	GGGG 694
Db	290	GGCTCAAGCTGTAATCCAGCACTTGGGGCGAGGGGGGGGGGGGG	GGGG 231
Qy	695	GGAGTCAAGGCCACCTGCGCAACATGGTAACTCTGCTCTGCTCTG	CTA 754
Db	230	GGAGTCAAGGCCACCTGCGCAACATGGTAACTCTGCTCTGCTCTG	CTA 171
Qy	755	TAGCCAGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	GCTG 814
Db	170	TAGCCAGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	GCTG 111
Qy	815	ATCGCTTGAAACCAGAGGGCGACGTTGGCTGCTGCTGCTGCTG	CTG 874
Db	110	ATCGCTTGAAACCAGAGGGCGACGTTGGCTGCTGCTGCTGCTG	CTG 51
Qy	875	CTGGCGACAGAGGTGAGCTCATCTCACACA 907	
Db	50	CTGGCGACAGAGGTGAGCTCATCTCACACA 18	
RESULT 2		Query Match	51.8%; Score 470; DB 2; Length 470;
BF914480/c		Best Local Similarity	100.0%; Pred. No. 5.4e-67;
LOCUS	BF914480	MATCHES	470 bp mRNA linear EST 18-JAN-2001
DEFINITION	IL3-UT0114-301100-358-E10 UT0114 Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BF914480		
VERSION	BF914480.1		
KEYWORDS	EST.		
SOURCE			
ORGANISM	Homo sapiens (human)		
HOMO SAPIENS			
BURKARTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI; MAMMALIA; EUCHERIA; PRIMATES; CATTARRINI; HOMINIDAE; HOMO.			
REFERENCE	1 (bases 1 to 470)		
AUTHORS	Eduardo Neto, E., Carla Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.P., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.		
RESULT 3			

BF915910/c	BF915910	470 bp	mRNA	linear	EST 18-JAN-2001	Db	230	GTTGAGCTGAAGGGCTTGGCCAGGTCAAGGTGGGGCGAACATCCATAAGAA	171
LOCUS	BF915910					OY	390	CCAGAGGCTCTGCCGCCGCCAGACGTCATCTGCCAGCTCTCTGCTGGCCGT	449
DEFINITION	IL3-UT0114-081200-366-E06	U0114	Homo sapiens	CDNA,	mRNA sequence.				
ACCESSION	BF915910								
VERSION	BF915910.1								
KEYWORDS	EST.								
SOURCE	Homo sapiens	(human)							
ORGANISM	Homo sapiens								
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed								
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)								
MEDLINE	2022663								
PUBMED	10737800								
COMMENT	Contact: Simpson A.J.G.								
FEATURES	Source								
	Ludwig Institute for Cancer Research								
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,								
	Brazil								
	Tel: +55-11-2704922								
	Fax: +55-11-2707001								
	Email: asimpson@ludwig.org.br								
	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL3&t2=IL3-UT0114-081200-366-E06&t3=2000-12-08&t4=1)								
	Seq primer: Puc 18 forward								
	High quality sequence stop: 455.								
	Location/Qualifiers								
	1. .470								
	/organism="Homo sapiens"								
	/mol_type="mRNA"								
	/db_xref="taxon:9606"								
	/dev_stage="Adult"								
	/clone_lib="UT0114"								
	/note="Organ: uterus tumor; Vector: puc18; Site_1: Small; Site_2: Small; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."								
ORIGIN									
Query Match	51.8%	; Score 470;	DB 2;	Length 470;					
Best Local Similarity	100.0%	; Pred. No. 5.4e-67;	Matches 470;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
QY	90	AGATAACTCTGAGGGAGGACGCCATAGGGAGTACTCTCTGCCCTCCACCTCCCC	149						
Db	470	AGATAACTCTGAGGGAGGACGCCATAGGGAGTACTCTCTGCCCTCCACCTCCCC	411						
QY	150	GGTGTTCACGGGGCGCTGGTGCCTCTCTGGCAGAGGTCTCTGGCTGGCC	209						
Db	410	GGTGTTCACGGGGCGCTGGCAGAGGTCTCTGGCTGGCC	351						
QY	210	GGAGCTCACGACTCCAGCCTTGTTACCGAGAGGAGACTTGCAAGGGCTGGAGATG	269						
Db	350	GGAGCTCACGACTCCAGCCTTGTTACCGAGAGGAGACTTGCAAGGGCTGGAGATG	291						
QY	270	GTCGGGGAGTCACACAGAGTGGCGAGGAGGAGACTTCTTGGCTG	329						
Db	290	GTCGGGGAGTCACACAGAGTGGCGAGGAGACTTCTTGGCTG	231						
QY	330	GTTGGACAGTAGAGGGCTTGGCCAGGTGGGGGGCAACTCATAAAGAA	389						

JOURNAL Unpublished (1997)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LILN; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 456.

FEATURES
SOURCE

Location/Qualifiers

1. . 480

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:604024"

/db_xref="taxon:9606"

/clone="IMAGE:810034"

/sex="Female"

/tissue="Type="ovarian tumor"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares ovary tumor NbHOT"

/note="Organ: ovary; Vector: pRT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTACCACTCGAGGAGGGAGCCCGCGTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 50.5%; Score 458; DB 1; Length 480;
 Best Local Similarity 99.6%; Pred. No. 4.8e-65; Mismatches 0; Indels 2; Gaps 2;
 Matches 480; Conservative 0; MisMatches 0; Indels 2; Gaps 2;

QY

113 ATAGGGGAACTCTACTCCCTCCACCTGCCCTGGGTCAGGGTGCCCTGGTCC 172

480 ATAGGGGAACTCTACTCCCTCCACCTGCCCTGGGTCAGGGTGCCCTGGTCC 421

QY

173 TCTCTTCCGAGAGAGGTCTCTGGTCAAGGGAGCAGAGGAGCTCAAGACTCC 232

420 TCTCTTCCGAGAGAGGTCTCTGGTCAAGGGAGCAGAGGAGCTCAAGACTCC 361

QY

233 TGTGTTACCGAGAGAGACTTGCAAGCTGTCGGATGTCGGAGAGCTCACAGCTG 292

360 TGTGTTACCGAGAGAGACTTGCAAGCTGTCGGATGTCGGAGAGCTCACAGCTG 301

QY

293 GGGGGAGGGGAGGGAGAGCTGTCGGTGTGAGCTAGTAGGGGCTTG 352

300 GGGGGAGGGGAGGGAGAGCTGTCGGTGTGAGCTAGTAGGGGCTTG 241

QY

353 CGAGTCAGGGAGGGAGGGAGCTCATTAAGAACCAAGGGCTGGGGCCAGCA 412

340 CGAGTCAGGGAGGGAGGGAGCTCATTAAGAACCAAGGGCTGGGGCCAGCA 182

QY

413 CAGAGTCATCTGGGGAGCTCTCTGCGCTGGGGAGCTGGGGCTGGGGCTT 472

181 CAGAGTCATCTGGGGAGCTCTCTGCGCTGGGGAGCTGGGGCTGGGGCTT 122

QY

473 TGTGCGCTGAAACCAACCAACAGGGCTGGGGCTGGGGCTGGGGCTGGGGCTT 532

121 TGTGCGCTGAAACCAACCAACAGGGCTGGGGCTGGGGCTGGGGCTGGGGCTT 63

QY

533 AATTCCTAACCTCTCTCTCTAGGACCCAAAGAGCTTATGATCATTTGATT 592

62 AATTCCTAACCTCTCTCTAGGACCCAAAGAGCTTATGATCATTTGATT 3

QY

593 AC 594

2 AC 1

RESULT 7

REFERENCE

AUTHORS

VERSION

KEYWORDS

SOURCE

ORGANISM

COMMENT

TITLE

JOURNAL

COMMENT

RESULT 8

Db 186 GGCCACAGAGCATCTGCCGCCTCTCTCTGCGCAGTGGAGTCAGGAGGG 127
 QY 468 GCGTTGTCGCAAGTAACCCAGGGTGTGCTGCGGCCATGGCCCTGCTTAG 527
 Db 126 GGCTTGTCGCAAGTAACCCAGGGTGTGCTGCGGCCATGGCCCTGCTTAG 68
 QY 528 GCAGCAATTCTCAACCTCTGCTCAGGACCCAAAGAGGCTTCATGATATGA 587
 Db 67 GCAGCAATTCTCAACCTCTGCTCAGGACCCAAAGAGGCTTCATGATATGA 8
 QY 588 TTTCAC 594
 Db 7 TTTTAC 1

SOURCE
 ORGANISM
 Locus AA399124 402 bp mRNA linear EST 16-MAY-1997
 DEFINITION IMAGE:725642 5', mRNA sequence.
 ACCESSION AA399124
 VERSION AA399124.1 GI:2052862
 KEYWORDS EST.
 COMMENT Homo sapiens (human)
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS 1 (bases 1 to 402)
 Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
 Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
 Moore,B., Scheilberg,K., Steptoe,M., Tan,F., Theising,B.,
 White,Y., Wylie,T., Waterston,R. and Wilson,R.
 TITLE WashU-Merck EST Project 1997
 JOURNAL Unpublished (1997)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LILN; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 279.

FEATURES source

1. .402
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:5937549"
 /db_xref=taxon:9606"
 /clone="IMAGE:725642"
 /sex="Female"
 /tissue_type="ovarian tumor"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares ovary tumor NBNOT"
 /note="Organ: ovary; Vector: pTV13D (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATTCTGAGTGGAGCGGCCGGTTTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pTV13 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bonaldo."

ORIGIN

Query Match 40.7%; Score 369; DB 1; length 402;
 Best Local Similarity 99.3%; Pred. No. 1.6e-50;
 Matches 402; Conservative 0; Mismatches 0; Indels 3; Gaps 3;
 QY 190 TCTCTGGTCAAGGACGAGGAGGCTCACAGACTTCAGCCCTTGTACGGAGGACA 249

RESULT 9

Db 480 AGGCTGATTGCTGGCCACTGGGAGTGGCTGACGTTGAGCTTCAGGCTTCAGGAGG 549
 QY 250 CTTGCGAAGTCCAGCGAGTGGCTCGGAGTCACACAGACTCGGGAGGGAGGG 309
 Db 342 CTGGCAAGTCCAGCGAGTGGCTGAGCTGCGAACAGACTCGGGAGGGAGGG 283
 QY 310 GGACAGTCTGTTGCTGGTGGAGACGTAAGGCTTGGCCAGGGTGGGG 369
 Db 282 GGACAGTCTGTTGCTGGTGGAGACGTAAGGCTTGGCCAGGGTGGGG 223
 QY 370 GCGGAACTCCATAAAGAACCCAGAGGCTGGGGCCACAGACATGCCAG 429
 Db 222 GCGCAAATCCATAAAGAACCCAGAGGCTGGGGCCACAGACATGCCAG 164
 QY 430 CTCCCTGCTGCTGCCACTGGGAGTGGCCACAGGGTGGGGCTTGTGCAAGAACAC 489
 Db 103 AGGCTGAGTTCGCGGCCAT-GTCCTGCTAGGGCAGGTTG 46
 QY 550 CTCTCAGGACCCAAAGACGCTTCATGATCTATGTTAC 594
 Db 163 CTCTCAGGACCCAAAGACGCTTCATGATCTATGTTAC 1

SOURCE
 ORGANISM
 Locus AA481356 360 bp mRNA linear EST 08-AUG-1997
 DEFINITION IMAGE:756485 5', mRNA sequence.
 ACCESSION AA481356
 VERSION AA481356.1 GI:2210308
 KEYWORDS EST.
 COMMENT Homo Sapiens (human)
 Homo Sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS 1 (bases 1 to 360)
 Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
 Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
 Moore,B., Scheilberg,K., Steptoe,M., Tan,F., Theising,B.,
 White,Y., Wylie,T., Waterston,R. and Wilson,R.
 TITLE WashU-Merck EST Project 1997
 JOURNAL Unpublished (1997)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LILN; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 219.

FEATURES source

1. .360
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:756485"
 /sex="Female"
 /tissue_type="ovarian tumor"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares ovary tumor NBNOT"
 /note="Organ: ovary; Vector: pTV13D (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATTCTGAGTGGAGCGGCCGGTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pTV13 vector

(Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo.

ORIGIN

Query Match 37.9%; Score 344.2; DB 1; Length 360;
Best Local Similarity 98.9%; Pred. No. 1.8e-46; Mismatches 3; Indels 1; Gaps 1;
Matches 357; Conservative 0; Note: "Organ: Stomach; Vector: pTR73-Pac; Site_1: BCOI; Site_2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-805. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."

ORIGIN

Query Match 35.9%; Score 334.4; DB 4; Length 547;
Best Local Similarity 99.7%; Pred. No. 6.3e-45; Mismatches 1; Indels 0; Gaps 0;
Matches 335; Conservative 0; Note: "Organ: Stomach; Vector: pTR73-Pac; Site_1: BCOI; Site_2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-805. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."

RESULT 10

BM854082 BM854082 547 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST013380 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-145-D09
DEFINITION 5', mRNA sequence.
VERSION BM854082.1 GI:19210481

ACCESSION BM854082
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

JOURNAL Unpublished
COMMENT Contact: Kim YS
AUTHORS 1 (bases 1 to 547)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.B., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
TITLE C2C Frontier Korean EST Project 2001

JOURNAL Unpublished
COMMENT Contact: Kim YS
AUTHORS 1 (bases 1 to 547)
Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baita, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.P., de Souza, S.J. and
Simpson, A.J.G.

JOURNAL Unpublished
COMMENT Contact: Simpson A.J.G.
AUTHORS 1 (bases 1 to 547)
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-704922
Fax: +55-11-2707001

RESULT 11

BF963567 BF963567 511 bp mRNA linear EST 22-JAN-2001
LOCUS PMI-NNI1207-211200-013-d11 NN1207
DEFINITION Homo sapiens cDNA, mRNA Sequence.
VERSION BF963567.1 GI:12380751
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

JOURNAL Unpublished
COMMENT Contact: Kim YS
AUTHORS 1 (bases 1 to 511)
Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baita, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.P., de Souza, S.J. and
Simpson, A.J.G.

JOURNAL Unpublished
COMMENT Contact: Simpson A.J.G.
AUTHORS 1 (bases 1 to 511)
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-704922
Fax: +55-11-2707001

FEATURES
source
1. .54/
/organism="Homo sapiens"
/mol_type="mRNA"
/ab_xref="axxon:9606"
/clone="S22SNU16n1-145-D09"
/sex="P"
/tissue_type="Abcites"
/cell_type="Lymphoblast-like"

	MEDLINE PUBLMED COMMENT	20202633 1073700 Email: astimpson@ludwig.org.br This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM1&t2=NN1207-211200-013-d11&t3=2000-12-21&t4=1)
FEATURES source		Seq primer: puc 18 forward High quality sequence stop: 511. Location/Qualifiers 1. -511 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_lib="NN1207"
Query Match		/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-Library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN		Best Local Similarity 99.1%; Pred. No. 1.3e-40; Length 511; Matches 330; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
Qy		1 GGACTCTGAGGTCCAAAGGGCTCTGACGCCCAAGAAGGGTTCACCTTGAC 369 GGACTCTGAGGTCCAAAGGGCTCTGACGCCCAAGAAGGGTTCACCTTGAC
Db		61 CCCTAGGGTGTGGATTGCTGGTTAACAGATAACCTGGGGAGGACCCATAGGGA 309 CCCTAGGGTGTGGATTGCTGGTTAACAGATAACCTGGGGAGGACCCATAGGGA
Qy		121 ATGCTACTCTCTGCCTTCACCCCTCGCTGTTACAGATAACCTGGGGAGGACCCATAGGGA 249 ATGCTACTCTCTGCCTTCACCCCTCGCTGTTACAGATAACCTGGGGAGGACCCATAGGGA
Db		180 310 181 GAGAGAGTGTCTGAGTCCAGGACCCAGGAGCAGTCACAGACTCCAGCCCTTGAC 189 GAGAGAGTGTCTGAGTCCAGGACCCAGGAGCAGTCACAGACTCCAGCCCTTGAC
Qy		130 241 181 GAGAGAGTGTCTGAGTCCAGGACCCAGGAGCAGTCACAGACTCCAGCCCTTGAC 189 GAGAGAGTGTCTGAGTCCAGGACCCAGGAGCAGTCACAGACTCCAGCCCTTGAC
Db		309 CCCTAGGGTGTGGATTGCTGGTTAACAGATAACCTGGGGAGGACCCATAGGGA 121 ATGCTACTCTCTGCCTTCACCTGGCTCTGGTTACGGGAGCCTCTCCCTCTGGCC 369 GGACTCTGAGGTCCAAAGGGTTCACCTGGCTCTGGTTACGGGAGCCTCTCCCTCTGGCC
Qy		180 249 181 GAGAGAGTGTCTGAGTCCAGGACCCAGGAGCAGTCACAGACTCCAGCCCTTGAC 189 GAGAGAGTGTCTGAGTCCAGGACCCAGGAGCAGTCACAGACTCCAGCCCTTGAC
Db		310 309 301 GCAGAGGGGAGCAGTCTGTGTCTGGTG 333 71 GCAGAGGGGAGCAGTCTGTGTCTGGTG 39
RESULT 12		
LOCUS		B1034628 511 bp mRNA linear EST 14-JUN-2001
DEFINITION		PM1-NN1207-050401-013-d11 NN1207 Homo sapiens cDNA, mRNA sequence.
ACCESSION		B1034628
VERSION		B1034628.1 GI:14441254
KEYWORDS		EST.
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ORGANISM		Homo sapiens (human)
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. (bases 1 to 511)
REFERENCE		1. Diaz Neto,E., Garcia Correa,R., Verlowski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordim,S., Costi,F.F., Goldman,G.H., Carvalho,A.P., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE		Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Qy		1 GGACTCTGAGGTCCAAAGGGCTCTGACGCCCAAGAAGGGTTCACCTTGAC 369 GGACTCTGAGGTCCAAAGGGCTCTGACGCCCAAGAAGGGTTCACCTTGAC
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Qy		130 249 130 309 130 121 ATGCTACTCTCTGCCTTCACCTGGCTCTGGTTACGGGAGCCTCTCCCTCTGGAC 130 369 GGACTCTGAGGTCCAAAGGGTTCACCTGGCTCTGGTTACGGGAGCCTCTCCCTCTGGAC
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Qy		241 GAGAGAGTGTCTGAGTCCAGGACCCAGGAGCAGTCACAGACTCCAGCCCTTGTAAC 129 GAGAGAGTGTCTGAGTCCAGGACCCAGGAGCAGTCACAGACTCCAGCCCTTGTAAC
Db		308 301 308 129 GAGAGAGTGTCTGAGTCCAGGACCCAGGAGCAGTCACAGACTCCAGCCCTTGTAAC 308 71 GCAGAGGGGAGCAGTCTGTGTGTCTGGTG 39
RESULT 13		
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DEFINITION		1700060100739 GRN_PRENU Homo sapiens cDNA 5', mRNA sequence.
ACCESSION		CN277578
KEYWORDS		CN277578.1 GI:47293992
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SOURCE		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. (bases 1 to 308)
REFERENCE		1. (bases 1 to 308)

AUTHORS	Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murrage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandlum, R., Lebkowski, J. and Stanton, L.W.	COMMENT	MIPS
JOURNAL	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation	CONTACT	Ingostaedter Landstr. 1, D-85764 Neuherberg, Germany
DOCUMENT	Contact: Brandenberger R	This is the 5' sequence of the clone insert	This is the 5' sequence of the clone insert
GERE	Regenerative Medicine	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
CONTRIBUTOR	Geron Corporation	sequenced by BMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.	sequenced by BMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
ADDRESS	230 Constitution Drive, Menlo Park, CA 94025, USA	No 81 sequence available.	No 81 sequence available.
TELEPHONE	Tel: 650 473 8658	This clone (DKFZp761H1914) is available at the RZPD in Berlin.	This clone (DKFZp761H1914) is available at the RZPD in Berlin.
FAX	Fax: 650 473 7760	Please contact the RZPD: Ressourcenzentrum, Haubnerweg 6, 14059 Berlin-Charlottenburg, Germany; Email: clone@rzpd.de.	Please contact the RZPD: Ressourcenzentrum, Haubnerweg 6, 14059 Berlin-Charlottenburg, Germany; Email: clone@rzpd.de.
EMAIL	Email: rbrandenberger@geron.com	location	location
LENGTH	Insert Length: 308 Std Error: 0.00.	FEATURES	FEATURES
SOURCE	Location/Qualifiers	Source	Source
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1. .308	/db_xref="taxon:9605"		
1. .308	/tissue_type="embryonic stem cell, retinoic acid and mitogen-treated HES cell line H7"		
1. .308	/clone_lib="GRN PREMU"		
1. .308	/note="Oligo dt printed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."		
RIGIN		FEATURES	FEATURES
Query Match	Score 304.8; DB 7; Length 308;	Source	Source
Best Local Similarity	99.4%; Pred. No. 5.1e-40;	ORGANISM	ORGANISM
Matches	306; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Homo sapiens	Homo sapiens
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PUBLISHED 10737800
 COMMENT Contact: Simpson A.J.G.
 laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gehtml2.pl?tl=PM&tt2=PM1-MT0198-191200-007-d11&t3=2000-12-19&t4=1>)
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 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
 ORIGIN

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Gencore version 5.1.6
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(without alignments)

10038.575 Million cell updates/sec

Title: US-09-989-733-398

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Maximum Match 100% summaries

Listing first 1500 summaries

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4: gb_om:*

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10: gb_ro:*

11: gb_sts:*

12: gb_xy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	907	100.0	907	AX362337 Sequence
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98	210.8	23.3	153225	2	AC13581	Homo sapi	C	171	209.2	23.1	99486	9	AC008938 Homo sapi	
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C 259	208.6	23.0	132805	9	HS339A18	c 332	207.8	22.9	181265	2	AC008821	
C 260	208.6	23.0	132820	9	HS103D20	c 333	207.8	22.9	184111	9	ALJ359763	
C 261	208.4	23.0	179627	9	AC113426	c 334	207.8	22.9	190765	9	283844	
C 262	208.4	23.0	197000	2	AC124859	c 335	207.8	22.9	210799	2	AC008147	
C 263	208.4	23.0	207751	2	AC112189	c 336	207.8	22.9	254533	2	CR762389	
C 264	208.4	23.0	301352	9	AC008902	c 337	207.6	22.9	31766	6	AX354725	
C 265	208.4	23.0	119072	9	ALJ36531	c 338	207.6	22.9	343456	9	AC019076	
C 266	208.4	23.0	126231	9	AC041339	c 339	207.6	22.9	38852	9	AC006261	
C 267	208.4	23.0	131990	9	AC008925	c 340	207.6	22.9	62219	2	AC132200	
C 268	208.4	23.0	133867	9	ALU53648	c 341	207.6	22.9	13456	9	ALU53648	
C 269	208.4	23.0	141923	9	AC010997	c 342	207.6	22.9	129430	9	AC008905	
C 270	208.4	23.0	144676	9	HS330013	c 343	207.6	22.9	129719	9	ALJ58113	
C 271	208.4	23.0	145388	9	ALJ72602	c 344	207.6	22.9	134793	9	ZB4469	
C 272	208.4	23.0	147364	9	AC110998	c 345	207.6	22.9	157950	9	Human DNA	
C 273	208.4	23.0	154348	9	AC059480	c 346	207.6	22.9	143756	9	AC009783	
C 274	208.4	23.0	163149	9	CNS01DS2	c 347	207.6	22.9	149577	9	AC009783	
C 275	208.4	23.0	163705	2	AC023774	c 348	207.6	22.9	150440	2	AC054750	
C 276	208.4	23.0	163830	2	AC068235	c 349	207.6	22.9	151581	2	AC009157	
C 277	208.4	23.0	163876	2	AC016402	c 350	207.6	22.9	157950	9	AX354725	
C 278	208.4	23.0	169326	9	AC009783	c 351	207.6	22.9	163567	2	AC020922	
C 279	208.4	23.0	171657	9	AC114876	c 352	207.6	22.9	164607	9	AC02201	
C 280	208.4	23.0	174591	9	AC109335	c 353	207.6	22.9	164846	9	AC005902	
C 281	208.4	23.0	174768	9	AC079191	c 354	207.6	22.9	165761	2	AC054750	
C 282	208.4	23.0	186750	9	AC146199	c 355	207.6	22.9	165770	9	AC023396	
C 283	208.4	23.0	187514	2	AC019267	c 356	207.6	22.9	169598	9	AC034303	
C 284	208.4	23.0	194523	9	AC018642	c 357	207.6	22.9	171007	2	AC136365	
C 285	208.4	23.0	213745	9	AC009712	c 358	207.6	22.9	173627	9	AC009511	
C 286	208.4	23.0	227137	9	AC058481	c 359	207.6	22.9	174612	9	AC009494	
C 287	208.4	23.0	243041	9	AC004388	c 360	207.6	22.9	176584	2	AC062010	
C 288	208.4	23.0	2916	6	AX335303	c 361	207.6	22.9	177834	9	AC018811	
C 289	208.4	23.0	2916	2	Sequence AX337621	c 362	207.6	22.9	177852	9	AC034283	
C 290	208.4	23.0	2916	12	HSU14573	c 363	207.6	22.9	179168	2	AC009071	
C 291	208.4	23.0	43288	9	HS361A3	c 364	207.6	22.9	179652	2	AC149616	
C 292	208.4	23.0	79516	9	AC004834	c 365	207.6	22.9	182643	2	AC002794	
C 293	208.4	23.0	88029	9	AC004938	c 366	207.6	22.9	185029	9	AC090707	
C 294	208.4	23.0	91907	9	AC131566	c 367	207.6	22.9	188833	9	AC018811	
C 295	208.4	23.0	98433	9	AC094983	c 368	207.6	22.9	189098	9	AC034283	
C 296	208.4	23.0	117336	9	AC093171	c 369	207.6	22.9	191162	9	AC009071	
C 297	208.4	23.0	131359	9	AC004883	c 370	207.6	22.9	193645	2	AC015951	
C 298	208.4	23.0	136431	9	AC131675	c 371	207.6	22.9	198650	9	AC0149616	
C 299	208.4	23.0	177322	9	AC022168	c 372	207.6	22.9	204082	9	AC005323	
C 300	208.4	23.0	159929	2	AC156973	c 373	207.6	22.9	205749	9	AC018718	
C 301	208.4	23.0	169604	9	AC083884	c 374	207.6	22.9	207264	9	AC140753	
C 302	208.4	23.0	172033	2	AC093171	c 375	207.6	22.9	209599	9	AC008865	
C 303	208.4	23.0	22.9	172237	2	AC131389	c 376	207.6	22.9	210067	9	AC015951
C 304	208.4	23.0	176141	9	AC136783	c 377	207.6	22.9	210455	9	AC0117438	
C 305	208.4	23.0	22.9	178401	9	AC016975	c 378	207.6	22.9	212292	9	AC013418
C 306	208.4	23.0	186210	9	AC007596	c 379	207.6	22.9	132710	9	AC035353	
C 307	208.4	23.0	192473	2	AC074915	c 380	207.4	22.9	142085	9	AC0159707	
C 308	208.4	23.0	192653	9	AC124781	c 381	207.4	22.9	147424	2	AC023116	
C 309	208.4	23.0	211531	9	AC006995	c 382	207.4	22.9	156348	9	AC059513	
C 310	208.4	23.0	246322	2	AC133966	c 383	207.4	22.9	158966	9	AC098951	
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C	385	207.4	22.9	169554	2	AC021379	Homo sapi	458	207	22.8	217615	2	AC083976	Homo sapi
C	386	207.4	22.9	175335	9	AC106872		459	207	22.8	227912	2	AC138900	Homo sapi
C	387	207.4	22.9	182428	9	AC036167	Homo sapi	460	207	22.8	241781	9	AC15097	Homo sapi
C	388	207.4	22.9	18376	9	AC100821	Homo sapi	461	207	22.8	250483	2	AC145086	Homo sapi
C	389	207.4	22.9	18571	9	AC133781	Homo sapi	462	206.8	22.8	69201	9	AC004109	Homo sapi
C	390	207.4	22.9	18502	9	ALJ39081	Human DNA	463	206.8	22.8	77425	9	AF068625	Homo sapi
C	391	207.4	22.9	188296	9	AC022324		464	206.8	22.8	88295	9	AC004612	Homo sapi
C	392	207.4	22.9	188470	2	AC093005		465	206.8	22.8	89352	9	AC006030	Homo sapi
C	393	207.4	22.9	191154	2	AC132150	Homo sapi	466	206.8	22.8	99108	9	AC008666	Homo sapi
C	394	207.4	22.9	19394	9	AC114730	Homo sapi	467	206.8	22.8	10148	9	AC006146	Homo sapi
C	395	207.4	22.9	196592	9	CNS0008		468	206.8	22.8	11604	9	AF258245	Homo sapi
C	396	207.4	22.9	20711	2	AC133960		469	206.8	22.8	121717	9	AL445488	Homo sapi
C	397	207.4	22.9	206887	9	ALJ38898		470	206.8	22.8	136682	9	AL731574	Human DNA
C	398	207.4	22.9	207983	9	AC009960		471	206.8	22.8	149790	9	AC022106	Homo sapi
C	399	207.4	22.9	218921	9	AC08738		472	206.8	22.8	154577	9	AL357046	Homo sapi
C	400	207.4	22.8	47167	9	HST57P12		473	206.8	22.8	161164	2	AC022278	Homo sapi
C	401	207.2	22.8	57084	2	AC129892		474	206.8	22.8	167278	9	AP002806	Homo sapi
C	402	207.2	22.8	77080	9	AC114766		475	206.8	22.8	16905	9	AC096537	Homo DNA
C	403	207.2	22.8	9347	9	AL157373		476	206.8	22.8	166640	9	AC123779	Homo sapi
C	404	207.2	22.8	100719	9	BX255925		477	206.8	22.8	172614	9	AL929102	Human DNA
C	405	207.2	22.8	121909	9	HSU492P14		478	206.8	22.8	173403	9	BS000114	Pan trogl
C	406	207.2	22.8	130526	2	AP000715		479	206.8	22.8	174521	2	AC127468	Papio anu
C	407	207.2	22.8	138046	2	AC068478		480	206.8	22.8	175802	9	AC040179	Homo sapi
C	408	207.2	22.8	147534	9	AC068622		481	206.8	22.8	176629	9	AC08841	Homo sapi
C	409	207.2	22.8	151889	9	AC084250		482	206.8	22.8	177257	2	AL807789	Homo sapi
C	410	207.2	22.8	154339	2	AC090175		483	206.8	22.8	184886	9	AC016550	Homo sapi
C	411	207.2	22.8	167102	9	AC084017		490	206.8	22.8	195257	9	AL353505	Homo sapi
C	412	207.2	22.8	170722	9	AC087847		491	206.6	22.8	193132	2	AC025743	Homo sapi
C	413	207.2	22.8	170877	2	AC025610		492	206.6	22.8	198772	9	AC087192	Homo sapi
C	414	207.2	22.8	171035	9	AC016178		493	206.6	22.8	199208	9	AC019236	Homo sapi
C	415	207.2	22.8	172403	2	AC017061		494	206.6	22.8	205819	2	AC10605	Homo sapi
C	416	207.2	22.8	179317	9	AC021205		495	206.6	22.8	209593	9	CNS01R13	Homo sapi
C	417	207.2	22.8	184336	9	AC012499		496	206.6	22.8	331864	9	AF049895	Homo sapi
C	418	207.2	22.8	193811	2	AC148832		497	206.6	22.8	43913	9	AL46023	Pan trogl
C	419	207.2	22.8	202856	9	AC027374		498	206.6	22.8	57494	9	BS000189	Homo sapi
C	420	207.2	22.8	210133	2	AC013564		499	206.6	22.8	113109	9	AC57061	Homo sapi
C	421	207.2	22.8	2466	9	DR9927		500	206.6	22.8	76792	9	AC023161	Homo sapi
C	422	207.2	22.8	38906	9	BX842243		501	206.6	22.8	83731	2	AC079147	Homo sapi
C	423	207.2	22.8	39852	9	AC06128		502	206.6	22.8	96608	9	HS301813	Homo sapi
C	424	207.2	22.8	41530	9	AC005785		503	206.6	22.8	127883	2	AL136141	Homo sapi
C	425	207.2	22.8	46775	9	HSU738A13		504	206.6	22.8	129577	9	AC004659	Homo sapi
C	426	207.2	22.8	65128	9	AC073188		505	206.6	22.8	141000	9	AC121756	Homo sapi
C	427	207.2	22.8	75354	9	AC048340		506	206.6	22.8	16879	9	AC106854	Homo sapi
C	428	207.2	22.8	78367	9	AC092028		507	206.6	22.8	170491	9	AC008859	Homo sapi
C	429	207.2	22.8	83787	9	AC073009		508	206.6	22.8	17883	2	AL136141	Homo sapi
C	430	207.2	22.8	87386	9	AC133750		509	206.6	22.8	18078	9	AC005914	Homo sapi
C	431	207.2	22.8	87558	9	AC068768		510	206.6	22.8	18072	2	AC010722	Homo sapi
C	432	207.2	22.8	110000	2	AC014298		511	206.6	22.8	143060	9	AL929472	Homo DNA
C	433	207.2	22.8	113112	9	AC011248		512	206.6	22.8	17545	9	AC126614	Homo sapi
C	434	207.2	22.8	118312	9	AC055713		513	206.6	22.8	184271	9	AL392046	Homo sapi
C	435	207.2	22.8	121353	2	AC023386		514	206.6	22.8	154754	9	AC048336	Homo sapi
C	436	207.2	22.8	12529	9	AF179295		515	206.6	22.8	18078	9	AC005094	Homo sapi
C	437	207.2	22.8	128667	9	HSU94B14		516	206.6	22.8	160723	9	AC010722	Homo sapi
C	438	207.2	22.8	133323	9	AC116115		517	206.6	22.8	16981	9	AC10386	Homo sapi
C	439	207.2	22.8	13984	9	AC006455		518	206.6	22.8	17766	9	AC00549	Homo sapi
C	440	207.2	22.8	149058	2	AC023065		519	206.6	22.8	163972	9	AC103987	Homo sapi
C	441	207.2	22.8	15278	2	AC079190		520	206.6	22.8	167998	2	AL353662	Homo sapi
C	442	207.2	22.8	17179	9	AC145098		521	206.6	22.8	159736	2	AC019305	Homo sapi
C	443	207.2	22.8	173391	9	AC090063		522	206.6	22.8	171990	9	AL137071	Homo DNA
C	444	207.2	22.8	208859	9	AC084083		523	206.6	22.8	172868	2	AC016556	Homo sapi
C	445	207.2	22.8	179759	2	AC133268		524	206.6	22.8	173766	9	AC004049	Homo sapi
C	446	207.2	22.8	181864	9	ALJ53743		525	206.6	22.8	175827	9	AC133987	Homo sapi
C	447	207.2	22.8	191280	2	AC087389		526	206.6	22.8	177444	9	AC014668	Homo sapi
C	448	207.2	22.8	193519	2	AC023123		527	206.6	22.8	178384	2	AL591026	Homo sapi
C	449	207.2	22.8	201886	2	AC140511		528	206.6	22.8	180166	2	AC011899	Homo sapi
C	450	207.2	22.8	207050	9	AC010431		529	206.6	22.8	173048	2	AC016556	Homo sapi
C	451	207.2	22.8	21810	2	AC026112		530	206.6	22.8	185688	2	AC018805	Homo sapi
C	452	207.2	22.8	2181861	9	ALJ35793		531	206.6	22.8	187174	9	AC006241	Homo sapi
C	453	207.2	22.8	218210	9	AC140179		532	206.6	22.8	191960	9	AC024765	Homo sapi
C	454	207.2	22.8	215808	9	AC140179		533	206.6	22.8	196203	9	AL353555	Homo sapi
C	455	207.2	22.8	215936	9	CNS05TC		534	206.6	22.8	200464	2	AC148611	Macaca mulu
C	456	207.2	22.8	216749	9	AC104319		535	206.6	22.8	205793	9	AC026333	Homo sapi
C	457	207.2	22.8	216789	9	AC006534		536	206.6	22.8	225952	2	AL513473	Homo sapi

531	206.4	22.8	3621	9	AY204748	Homo sapi	c	604	206.2	22.7	187908	9	HS495010
532	206.4	22.8	28420	9	AL162391	Human DNA	c	605	206.2	22.7	188666	9	AC018211
533	206.4	22.8	35666	9	BX119906	Human DNA	c	606	206.2	22.7	12618	9	AC029111
534	206.4	22.8	59356	9	AC115109	Human DNA	c	607	206.2	22.7	200000	9	AP000512
535	206.4	22.8	78415	9	BS001611	Pan trogl	c	608	206.2	22.7	200430	9	AC011500
536	206.4	22.8	96594	6	AK095647	Sequence	c	609	206.2	22.7	201197	2	HS424112
537	206.4	22.8	99592	9	AP263284	Homo sapi	c	610	206.2	22.7	217035	9	AC099669
538	206.4	22.8	104658	9	AP006284	Homo sapi	c	611	206.2	22.7	220007	2	AC148335
539	206.4	22.8	114517	9	AL158152	Human DNA	c	612	206.2	22.7	339165	2	AC078987
540	206.4	22.8	119951	2	AC025267	Homo sapi	c	613	206	22.7	50564	9	AY338490
541	206.4	22.8	120044	9	AL590116	Human DNA	c	614	206	22.7	51841	2	AC024281
542	206.4	22.8	145333	2	AC013822	Homo sapi	c	615	206	22.7	52459	9	AF228703
543	206.4	22.8	151989	9	AC027139	Homo sapi	c	616	206	22.7	55256	9	HSJ735018
544	206.4	22.8	158013	9	AC131934	Human DNA	c	617	206	22.7	73029	9	HSBA33957
545	206.4	22.8	155339	9	AL138721	Human DNA	c	618	206	22.7	79555	9	AL583856
546	206.4	22.8	157242	2	AC083821	Homo sapi	c	619	206	22.7	82517	9	HS341D10
547	206.4	22.8	159593	2	AC007924	Homo sapi	c	620	206	22.7	82964	9	AL604028
548	206.4	22.8	160573	9	AC119676	Homo sapi	c	621	206	22.7	97559	9	AL356748
549	206.4	22.8	170562	2	AC087784	Homo sapi	c	622	206	22.7	101720	9	AC005006
550	206.4	22.8	171818	9	AC063962	Homo sapi	c	623	206	22.7	10584	9	AC103959
551	206.4	22.8	172163	9	AC134866	Human DNA	c	624	206	22.7	109576	9	CR72982
552	206.4	22.8	173999	9	AC097501	Human DNA	c	625	206	22.7	14327	9	AC114302
553	206.4	22.8	183301	2	AC092487	Homo sapi	c	626	206	22.7	149714	2	AC144499
554	206.4	22.8	187004	9	AC084082	Homo sapi	c	627	206	22.7	151933	2	AC071199
555	206.4	22.8	188639	9	AC011236	Homo sapi	c	628	206	22.7	154850	9	AC055711
556	206.4	22.8	194746	2	AC145544	Human DNA	c	629	206	22.7	15559	2	AL133336
557	206.4	22.8	210336	9	AC064433	Homo sapi	c	630	206	22.7	15665	9	AL11749
558	206.4	22.8	213527	9	AL732274	Human DNA	c	631	206	22.7	15620	2	AP002442
559	206.4	22.8	241304	9	AL954220	Pan trogl	c	632	206	22.7	149714	2	AC009314
560	206.4	22.8	250529	9	ALR000558	Human DNA	c	633	206	22.7	161794	9	AC021755
561	206.4	22.8	4936	9	AP134406	Human DNA	c	634	206	22.7	16571	9	AC020687
562	206.4	22.8	56270	9	AC117435	Homo sapi	c	635	206	22.7	171309	9	AC012146
563	206.4	22.8	71118	9	AL132442	Human DNA	c	636	206	22.7	191764	9	AC025168
564	206.4	22.8	72038	9	AL591166	Human DNA	c	643	206	22.7	193879	2	AC140510
565	206.4	22.8	73574	9	CR788220	Human DNA	c	644	206	22.7	19894	9	AC114781
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573	206.4	22.7	86397	9	AC117435	Homo sapi	c	646	206	22.7	185571	9	AC133781
574	206.4	22.7	104755	9	BX908728	Human DNA	c	647	206	22.7	191414	2	AC144518
575	206.4	22.7	105034	9	HSU047A17	Human DNA	c	648	206	22.7	191764	9	AC087624
576	206.4	22.7	110000	2	AL031785_0	Pan trogl	c	649	205.8	22.7	19879	2	AC002357
577	206.4	22.7	130666	9	BX294172	Homo sapi	c	650	205.8	22.7	198894	9	AC040435
578	206.4	22.7	121212	9	HS135L22	Human DNA	c	651	205.8	22.7	194516	2	AC026681
579	206.4	22.7	123554	9	AB023049	Human DNA	c	652	205.8	22.7	19451	2	AC115848
580	206.4	22.7	129552	9	HS091327	Human chrom	c	653	205.8	22.7	195956	2	AC009506
581	206.4	22.7	129947	9	HS65N24	Human DNA	c	654	205.8	22.7	195956	2	AC104955
582	206.4	22.7	130553	9	AL045333	Human DNA	c	655	205.8	22.7	195956	2	AC114730
583	206.4	22.7	130666	9	AL053882	Human DNA	c	656	205.8	22.7	195956	2	AC040435
584	206.4	22.7	137703	9	AC020982	Homo sapi	c	657	205.8	22.7	197075	9	AC00362
585	206.4	22.7	14702	9	AC02476	Pan trogl	c	658	205.8	22.7	197375	9	AC148448
586	206.4	22.7	147603	9	AL157078	Human DNA	c	659	205.8	22.7	197381	9	AC073841
587	206.4	22.7	149181	9	AC021813	Homo sapi	c	660	205.8	22.7	197557	9	AX695587
588	206.4	22.7	157042	9	AC105001	Homo sapi	c	661	205.8	22.7	19873	9	294801
589	206.4	22.7	158608	9	CNS05TDJ	Human DNA	c	662	205.8	22.7	118631	9	AC008888
590	206.4	22.7	161970	9	AP005660	Homo sapi	c	663	205.8	22.7	130403	9	AC010289
591	206.4	22.7	162454	9	AC011008	Human DNA	c	664	205.8	22.7	137022	9	AC027616_04
592	206.4	22.7	163444	2	AC025866	Homo sapi	c	665	205.8	22.7	139072	9	AB020878
593	206.4	22.7	164168	9	AL135927	Human DNA	c	666	205.8	22.7	14455	9	AL135341
594	206.4	22.7	164179	9	AC007227	Homo sapi	c	667	205.8	22.7	118873	9	HS1184F4
595	206.4	22.7	170107	2	AC151445	Panzo annu	c	668	205.8	22.7	146515	2	AC146981
596	206.4	22.7	171467	9	AL449223	Human DNA	c	669	205.8	22.7	15567	9	AC017349
597	206.4	22.7	171627	9	AL662297	Human DNA	c	670	205.8	22.7	178183	2	AC015957
598	206.4	22.7	175945	2	AC022147	Homo sapi	c	671	205.8	22.7	158103	9	AC0040485
599	206.4	22.7	179146	9	AC07852	Homo sapi	c	672	205.8	22.7	16237	9	AC016411
600	206.4	22.7	179854	2	AC149454	Panzo annu	c	673	205.8	22.7	16243	9	CHS01DU
601	206.4	22.7	180347	9	AC009415	Homo sapi	c	674	205.8	22.7	164725	9	AC0092938
602	206.4	22.7	184557	2	AC119554	Panzo annu	c	675	205.8	22.7	16657	9	AP05118
603	206.4	22.7	185617	9	AL662848	Human DNA	c	676	205.8	22.7	168064	2	AC019160

C	677	205.8	22.7	16964	2	AC023767	C	750	205.6	22.7	193643	9	AC01864
C	678	205.8	22.7	169979	2	AC013700	C	751	205.6	22.7	197000	2	AC124859
C	679	205.8	22.7	171812	9	AC013399	C	752	205.6	22.7	202815	9	AF271169
C	680	205.8	22.7	174839	9	AL157395	C	753	205.6	22.7	209859	9	AC084083
C	681	205.8	22.7	175195	2	AP001319	C	754	205.6	22.7	209870	9	AC10431
C	682	205.8	22.7	178235	9	AC060768	C	755	205.6	22.7	215150	9	AC026891
C	683	205.8	22.7	178625	9	AC106017	C	756	205.6	22.7	218074	9	AC023283
C	684	205.8	22.7	178975	2	AC023222	C	757	205.6	22.7	218630	2	AC148892
C	685	205.8	22.7	179272	2	AC059149	C	758	205.6	22.7	220458	9	AC010320
C	686	205.8	22.7	179372	2	AC040922	C	759	205.6	22.7	278310	2	AC069592
C	687	205.8	22.7	179511	9	AC025283	C	760	205.4	22.6	2619	6	AX430468
C	688	205.8	22.7	179581	4	AC009397	C	761	205.4	22.6	32638	2	AC146707
C	689	205.8	22.7	182301	9	AC012498	C	762	205.4	22.6	41385	9	AC14836
C	690	205.8	22.7	182431	9	AC068380	C	763	205.4	22.6	56516	6	BD19612
C	691	205.8	22.7	186115	9	AC008474	C	764	205.4	22.6	565564	9	AC013220
C	692	205.8	22.7	188100	2	AC034780	C	765	205.4	22.6	62799	2	AC114687
C	693	205.8	22.7	188460	9	AC010542	C	766	205.4	22.6	81403	9	AC024849
C	694	205.8	22.7	188560	4	AC141415	C	767	205.4	22.6	95360	9	AC146707
C	695	205.8	22.7	190025	2	AC140415	C	768	205.4	22.6	96594	6	AC14836
C	696	205.8	22.7	193212	9	AC004370	C	769	205.4	22.6	96865	9	AC138884
C	697	205.8	22.7	193390	9	AC013730	C	770	205.4	22.6	97059	9	AC005800
C	698	205.8	22.7	194237	9	AC068870	C	771	205.4	22.6	102202	9	AC027679
C	699	205.8	22.7	195110	9	AC107943	C	772	205.4	22.6	104726	9	AC008097
C	700	205.8	22.7	195913	9	AL954236	C	773	205.4	22.6	109238	9	AC024849
C	701	205.8	22.7	198664	9	AP006256	C	774	205.4	22.6	116470	9	AX655779
C	702	205.8	22.7	207901	2	AC147043	C	775	205.4	22.6	118234	9	AC138884
C	703	205.8	22.7	211305	9	AC079988	C	776	205.4	22.6	126327	9	AC005252
C	704	205.8	22.7	219190	9	CNS101D13	C	777	205.4	22.6	127006	9	AL138849
C	705	205.8	22.7	257967	4	AC032335	C	778	205.4	22.6	143146	9	HS1172N10
C	706	205.8	22.7	277335	2	AL499603	C	779	205.4	22.6	150563	9	AC019497
C	707	205.8	22.7	40111	11	BV190685	C	780	205.4	22.6	150645	9	AC11648
C	708	205.8	22.7	48217	9	AY190788	C	781	205.4	22.6	153471	9	AC095568
C	709	205.8	22.7	406449	9	AC003111	C	782	205.4	22.6	158276	9	AL355742
C	710	205.8	22.7	45459	2	AC006103	C	783	205.4	22.6	159376	9	HSU95742
C	711	205.6	22.7	75237	2	AC022935	C	784	205.4	22.6	142201	9	AC124248
C	712	205.6	22.7	131140	2	AC027474	C	785	205.4	22.6	143146	9	AC079855
C	713	205.6	22.7	110000	2	AL732359_00	C	786	205.4	22.6	155369	2	AC084228
C	714	205.6	22.7	110000	2	Continuation_12_OE	C	787	205.4	22.6	155989	9	AL355932
C	715	205.6	22.7	115043	9	AL663070	C	788	205.4	22.6	157676	9	AC027358
C	716	205.6	22.7	118405	9	AC012349	C	789	205.4	22.6	158257	9	AC005855
C	717	205.6	22.7	131140	2	AC020819	C	790	205.4	22.6	159305	9	AC026085
C	718	205.6	22.7	131147	9	AC124857	C	791	205.4	22.6	159978	2	AC139179
C	719	205.6	22.7	134950	2	AP002337	C	792	205.4	22.6	161309	9	AC10839
C	720	205.6	22.7	137233	2	AC090271	C	793	205.4	22.6	164026	2	AC143391
C	721	205.6	22.7	141007	2	AC025764	C	794	205.4	22.6	165307	2	AC148831
C	722	205.6	22.7	142520	9	HS620E11	C	795	205.4	22.6	165307	2	AC148831
C	723	205.6	22.7	151450	9	AC018679	C	796	205.4	22.6	165799	2	AC108013
C	724	205.6	22.7	151452	9	AP01894	C	797	205.4	22.6	165807	2	AL398107
C	725	205.6	22.7	152484	2	AC067992	C	798	205.4	22.6	167005	2	AC008822
C	726	205.6	22.7	153185	2	AC073228	C	799	205.4	22.6	167075	2	AC138884
C	727	205.6	22.7	155290	9	AL359175	C	800	205.4	22.6	168136	9	AP28957
C	728	205.6	22.7	160370	9	AC023464	C	801	205.4	22.6	169371	2	AC138902
C	729	205.6	22.7	170797	9	AC011379	C	802	205.4	22.6	169414	9	AC068707
C	730	205.6	22.7	170849	9	AC126366	C	803	205.4	22.6	169665	2	AC145566
C	731	205.6	22.7	172837	9	AL450304	C	804	205.4	22.6	170135	2	AC137873
C	732	205.6	22.7	174856	2	BX296555	C	805	205.4	22.6	172334	9	AC010550
C	733	205.6	22.7	175006	2	AC027589	C	806	205.4	22.6	172512	9	AC015903
C	734	205.6	22.7	176278	9	AC024028	C	807	205.4	22.6	172827	9	AC007216
C	735	205.6	22.7	176550	9	AL356356	C	808	205.4	22.6	173525	9	AC067893
C	736	205.6	22.7	178653	2	AC090088	C	809	205.4	22.6	177483	9	AC068333
C	737	205.6	22.7	178982	9	AP001591	C	810	205.4	22.6	180221	9	AC007277
C	738	205.6	22.7	179627	9	AC113426	C	811	205.4	22.6	180372	2	AC012939
C	739	205.6	22.7	179666	2	AC138145	C	812	205.4	22.6	181277	2	AC139478
C	740	205.6	22.7	180889	9	AC079986	C	813	205.4	22.6	181597	9	AC090515
C	741	205.6	22.7	184057	9	AP000753	C	814	205.4	22.6	182512	9	AC014777
C	742	205.6	22.7	184059	2	AC090382	C	815	205.4	22.6	183307	9	AC096539
C	743	205.6	22.7	184512	9	AC079804	C	816	205.4	22.6	183485	2	AC02578
C	744	205.6	22.7	184840	9	AC079907	C	817	205.4	22.6	183861	9	AC078816
C	745	205.6	22.7	184886	9	AC005358	C	818	205.4	22.6	184148	2	AC148725
C	746	205.6	22.7	184889	9	AL442125	C	819	205.4	22.6	184585	9	AC079465
C	747	205.6	22.7	185424	2	AC084709	C	820	205.4	22.6	184649	2	AC025196
C	748	205.6	22.7	191291	2	AC148313	C	821	205.4	22.6	185182	9	AC093423
C	749	205.6	22.7	192203	9	AC034102	C	822	205.4	22.6	185834	2	AC009632

923	205.4	22.6	185964	9	AC009399	896	205	22.6	84678	2	AC087464	Homo sapi
c	824	205.4	22.6	186112	2	AC069398	c	897	205	22.6	88018	9
c	825	205.4	22.6	189779	9	AL354733	c	898	205	22.6	90096	9
c	826	205.4	22.6	190483	2	AC148839	c	899	205	22.6	91224	9
c	827	205.4	22.6	19129	2	AL590872	c	900	205	22.6	94168	9
c	828	205.4	22.6	192126	9	DJ770M14	c	901	205	22.6	94635	9
c	829	205.4	22.6	196337	9	AC158975	c	902	205	22.6	95885	9
c	830	205.4	22.6	196221	2	AC090780	c	903	205	22.6	98876	9
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c	832	205.4	22.6	199330	2	AC148360	c	905	205	22.6	107842	9
c	833	205.4	22.6	199454	2	AC171780	c	906	205	22.6	107761	9
c	834	205.4	22.6	202168	2	AC092345	c	907	205	22.6	112351	9
c	835	205.4	22.6	204963	2	AC145617	c	908	205	22.6	112417	9
c	836	205.4	22.6	206337	9	AC126917	c	909	205	22.6	115888	9
c	837	205.4	22.6	209718	2	AC091099	c	910	205	22.6	123004	9
c	838	205.4	22.6	210888	2	AC137498	c	911	205	22.6	123657	9
c	839	205.4	22.6	210867	2	AC144878	c	912	205	22.6	124437	9
c	840	205.4	22.6	213481	9	AC134618	c	913	205	22.6	125495	9
c	841	205.4	22.6	213481	9	AC134618	c	914	205	22.6	129149	9
c	842	205.4	22.6	206516	9	AC134619	c	915	205	22.6	13414	2
c	843	205.4	22.6	225116	9	AC14619	c	916	205	22.6	13916	9
c	844	205.4	22.6	231334	2	AC148222	c	917	205	22.6	133154	9
c	845	205.4	22.6	237952	2	AC159116	c	918	205	22.6	138894	9
c	846	205.4	22.6	24844	2	AC134883	c	919	205	22.6	148859	9
c	847	205.4	22.6	328187	2	AC171939	c	920	205	22.6	142201	9
c	848	205.4	22.6	3016	6	AX41028	c	921	205	22.6	145551	9
c	849	205.4	22.6	3674	9	AP17523	c	922	205	22.6	147999	2
c	850	205.2	22.5	3251	9	HUMHDC	c	923	205	22.6	150720	9
c	851	205.2	22.6	73845	2	AL356478	c	924	205	22.6	154448	9
c	852	205.2	22.6	85138	9	AL137224	c	925	205	22.6	15386	9
c	853	205.2	22.6	88215	9	AC006963	c	926	205	22.6	153382	9
c	854	205.2	22.6	95240	9	AC007421	c	927	205	22.6	15551	9
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c	861	205.2	22.6	129169	2	AC020398	c	934	205	22.6	162440	2
c	862	205.2	22.6	142273	9	AL391994	c	935	205	22.6	166887	2
c	863	205.2	22.6	165531	2	AC003038	c	936	205	22.6	168015	2
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c	871	205.2	22.6	170269	9	AC030279	c	944	205	22.6	180104	9
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c	875	205.2	22.6	174559	9	AC015720	c	948	205	22.6	188295	9
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c	878	205.2	22.6	178902	2	AL513525	c	951	205	22.6	19433	9
c	879	205.2	22.6	178985	9	HS330819	c	952	205	22.6	227568	9
c	880	205.2	22.6	179221	9	AC114493	c	953	205	22.6	31283	9
c	881	205.2	22.6	185167	9	AC009077	c	954	204	22.6	3234	9
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c	889	205.2	22.6	204480	2	AC019083	c	962	204	22.6	104941	9
c	890	205.2	22.6	204769	2	AC150377	c	963	204	22.6	108316	6
c	891	205.2	22.6	213025	2	AC021159	c	964	204	22.6	11000	2
c	892	205.2	22.6	242913	9	AC15994	c	965	204	22.6	116506	9
c	893	205.2	22.6	16765	9	AL732409	c	966	204	22.6	122282	9
c	894	205.2	22.6	48832	9	HS301R23	c	967	204	22.6	126080	2
c	895	205.2	22.6	82251	9	AC004506	c	968	204	22.6	127399	9

969	204.8	22.6	138331	9	AC008798	Homo sapi	
970	204.8	22.6	135818	2	ALJ59965	Homo sapi	
C	971	204.8	22.6	136002	9	AC120024	Homo sapi
C	972	204.8	22.6	142373	9	ALG91994	Human DNA
C	973	204.8	22.6	147514	9	AC008521	Human DNA
C	974	204.8	22.6	155432	9	ALD9569	Human DNA
C	975	204.8	22.6	159191	9	AC009951	Human DNA
C	976	204.8	22.6	160550	9	AC130184	Macaca mulatta
C	977	204.8	22.6	165220	9	AC010323	Homo sapi
C	978	204.8	22.6	168227	9	AC118658	Homo sapi
C	979	204.8	22.6	168331	2	AC144998	Pan troglodytes
C	980	204.8	22.6	169193	2	AC068523	Homo sapi
C	981	204.8	22.6	169308	2	AC150910	Pan troglodytes
C	982	204.8	22.6	170423	9	AC018663	Human Chimp
C	983	204.8	22.6	174378	9	AC020983	Homo sapi
C	984	204.8	22.6	174502	2	AC110071	Homo sapi
C	985	204.8	22.6	175075	9	AC113346	Homo sapi
C	986	204.8	22.6	175226	9	AC002330	Homo sapi
C	987	204.8	22.6	177550	9	AC005874	Homo sapi
C	988	204.8	22.6	177864	9	ACR13471	Homo sapi
C	989	204.8	22.6	177978	9	AC009073	Homo sapi
C	990	204.8	22.6	177978	9	AC009126	Homo sapi
C	991	204.8	22.6	181923	9	AC022872	Homo sapi
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C	993	204.8	22.6	186047	9	AC074257	Homo sapi
C	994	204.8	22.6	189333	9	AC025678	Homo sapi
C	995	204.8	22.6	191684	9	AC146499	Pan troglodytes
C	996	204.8	22.6	192046	9	AC110772	Homo sapi
C	997	204.8	22.6	193101	2	AC009561	Homo sapi
C	998	204.8	22.6	195446	9	AC093709	Pan troglodytes
C	999	204.8	22.6	196446	2	AC074247	Homo sapi
C	1000	204.8	22.6	214422	9	AC06060	Human gestalt
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ORGANISM	Homo sapiens	OY	781 TAGTCCCGTACTCGGAGSCTGAGCAGAAGAACATCGCTGAACCCAGGGCGGACGT 840
REFERENCE	Bukiryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DB	781 TAGTCCCGTACTCGGAGSCTGAGCAGAAGAACATCGCTGAACCCAGGGCGGACGT 840
AUTHORS	Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watnabe,C.K. and Wood,W.I.	OY	841 TCGGTGAGGCCAGATCGGGCGCTGATTCCAGCCCTGGCAAGAGTGAGACTCCATC 900
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same	DB	841 TCGGTGAGGCCAGATCGGGCGCTGATTCCAGCCCTGGCAAGAGTGAGACTCCATC 900
JOURNAL	Patent: WO 0208288-A 97 31-JAN-2002; Genentech, Inc. (US)	OY	901 TCACAC 907
FEATURES	source	Db	901 TCACAC 907
ORIGIN			
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Db	61 CCTCTAGGGCTCTGATGTTGCTGTTAACAGATAACCTGAGGAGCCCTAGGG 120	SOURCE	Homo sapiens (human)
OY	121 ATCTACTCTCCCTCCCTTACCTGCTGGCTGTTAACAGATAACCTGAGGAGCTGGTCACCTTGAC 180	ORGANISM	Bukiryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Db	121 ATCTACTCTCCCTCCCTTACCTGCTGGCTGTTAACAGATAACCTGAGGAGCTGGTCACCTTGAC 180	REFERENCE	1 Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D., Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P., Grimaldi,C.J., Gurney,A.L., KJavvin,I., Napier,M.A., Pan,J., Roni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watnabe,C.K., Williams,B., Wood,W.I. and Zhang,Z.
OY	181 GAGAGAGTCTCTGGCTGGAGGAGGAGCTCACAGTCTCCAGCCCTTGTAAC 240	AUTHORS	the same
Db	181 GAGAGAGTCTCTGGCTGGAGGAGGAGCTCACAGTCTCCAGCCCTTGTAAC 240	TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding
OY	241 GAGAGAGACTTGCAGGAGCTTCAGGATGTTCCAGGAGCTGGACCTTGACC 300	JOURNAL	Patent: WO 0073454-A 398 07-DEC-2000;
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OY	301 GCGAGGGGGGAGCTGGTCTGTCGCTGCTGCTGAGCTAACAGGCTGTCAGTCA 360	source	Location/Qualifiers
Db	301 GCGAGGGGGGAGCTGGTCTGTCGCTGCTGAGCTAACAGGCTGTCAGTCA 360	OY	1 . 907
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Db	481 TAATACACAGCTGGTCTGGGGGCTGCTGCTGGAGCTGGAGCTGGAGCTGG 540	Best Local Similarity	100.0%; Pred. No. 1e-244;
OY	541 ACCTCTCTCTGAGGAGCCCAAGAGAGCTTCTTGTGATCTGATTTACCAT 600	Matches	0; Mismatches 0; Indels 0; Gaps 0;
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Db		Title	Wynan,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Oy	781 TATGCCCTGAGTACTCGGAGGGCTGAGGAGGAATGCCTTGACCCAGGGCGGAGCT	Journal	Direct Submission
Db	841 TCGGTGAGCCAGATGCGGCCCTGATTCGCGCTGGCGAGAAGTGGACTCCTCATC	Reference	Submitted (06-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
Oy	901 TCAACAC 907	Authors	4 (bases 1 to 101777)
Db	901 TCAACAC 907	Accession	Birren,B., Muzumori,C., Lander,E., Abouelleil,A., Allen,N., Anderson,S., Arachchi,H.M., Barna,N., Basien,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corrin,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,J., Grand-Pierre,N., Hafez,N., Haugian,D., Hagos,B., Hall,J., Horton,L., Huime,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Ton,K., Liu,G., Lui,A., Mabbett,R., MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrum,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicoll,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Rettig,R., Rice,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Strange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkatraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
REFERENCE	AC105210	Definition	AC105210 101777 bp DNA linear PRI 27-MAR-2003
LOCUS	Homo sapiens chromosome 8, clone RP11-18P12, complete sequence.	KeyWords	HTG
ACCESSION	AC105210	Source	Homo sapiens (human)
VERSION	AC105210.10	Organism	Homo sapiens
KEYWORDS		Reference	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 101777)	Authors	Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boinkgalter,B., Brown,A., Camarata,J., Coppolino,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heatord,A., Horton,L., Huime,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lamasabres,R., Landers,T., Lehoczky,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Major,J., Margolis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McCheeters,R., Meldrim,J., Menets,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Raymond,J., Retta,R., Roy,A., Santos,R., Schauer,S., Schupback,R., Roman,J., Roberti,M., Severy,P., Stojanovic,N., Straus,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Vassiliev,H., Vial,R., Vo,A., Wilson,B., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE	Unpublished	Journal	Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02111, USA
JOURNAL		Comment	On Mar 27, 2003 this sequence version replaced gi:28261622. All repeats were identified using RepeatMasker. Smit, A.P.F. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
REFERENCE	2 (bases 1 to 101777)	Source	Project: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: Sequencing genome.wi.mit.edu Center project name: L23062 Center clone name: 118_P_12
AUTHORS		Features	Only the middle 101.8 kilobases of this clone are being submitted. The remainder overlaps either accession number AC067930 [WIGGR project L1010] or accession number AC105219 [WIGGR project L23081].
TITLE		Source	Location/Qualifiers 1..101777 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="ttaxon:9606" /chromosome="8" /map="8" /clone="RP11-18P12" /clone_id="RPCI-11_Human_Male_BAC"
JOURNAL		repeat_region	repeat_region /rpt_family="G-rich" 1437..1559 /rpt_family="(CCCCCA)n"
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AUTHORS		repeat_region	repeat_region /rpt_family="G-rich" 6401..6553
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AUTHORS		repeat_region	repeat_region /rpt_family="MLT1B" 14312..14755
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RESULT 7 AC067930/c		

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Matches 907; Conservative 0; Mismatches 0; Indels 0;
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DEFINITION Homo sapiens chromosome 8, clone RP11-661A12, complete sequence.
ACCESSION AC067930
VERSION AC067930.7
KEYWORDS HTG.

ORGANISM	Homo sapiens	Smith,C., Spencer,B., Strange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Zuker,M.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	Ziel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Ziel,R., Zimmer,A. and Zody,M.
REFERENCE	1 (bases 1 to 174906)	Submitted (24-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02111, USA
AUTHORS	Birren,B., Nusbaum,C. and Lander,E.	Direct Submission
JOURNAL	Homo sapiens chromosome 8, clone RP11-661A12	Submitted (24-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02111, USA
REFERENCE	Unpublished	All repeats were identified using RepeatMasker: Smit, A.P.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RW/RepeatMasker.html
2 (bases 1 to 174906)		
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Campopiano,A., Castle,A., Chopek,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearlano,K., Dewart,V., Beda,F., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Ginde,S., Goyette,M., Graham,L., Boguslavsky,L., Boukhgatier,B., Brown,A., Burkett,G., Galagan,J., Gardyna,S., Ginde,S., Hagos,B., Heastad,A., Horton,L., Grand-Pierre,N., Grant,G., Murphy,T., Naylor,J., Norman,C.H., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Larocque,K., Lamazares,R., Landers,T., Lehozcy,J., Levine,R., Lieu,C., Liu,G., Locke,J., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McCork,K., McKernan,K., McPheebers,R., Meldrum,J., Menous,L., Minova,T., Miranda,C., Mlenga,V., Morrow,J., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,P., O'Neil,D., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.	
TITLE	Direct Submission	
JOURNAL	Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02111, USA	
REFERENCE	3 (bases 1 to 174906)	
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Chopek,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., Dearlano,K., Dewart,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzgerald,M., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Govertte,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Larocque,K., Lamazares,R., Landers,T., Lehozzy,J., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrum,J., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrum,J., Menous,L., Mihowa,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicoll,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,D., Raymond,C., Resta,R., Rieback,M., Riley,R., Rose,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,P., Strange-Thomann,N., Stojanovic,N., Strausse,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.	
TITLE	Direct Submission	
JOURNAL	Submitted (21-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02111, USA	
REFERENCE	4 (bases 1 to 174906)	
AUTHORS	Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgatier,B., Camarata,J., Chang,J., Chazaro,B., Chopek,Y., Colangelo,A., Cook,A., Cooke,P., Dearlano,K., Dewart,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzgerald,M., Gord,S., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Karatas,A., Kells,C., Larocque,K., Landers,T., Lehozzy,J., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Mattheus,C., McCarthy,M., Meldrum,J., Menous,L., Mihowa,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicoll,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Resta,R., Rieback,M., Riley,R., Rose,C., Romon,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,	
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RESULT 8 AC019122 DEFINITION Homo sapiens chromosome 8 clone RP11-545C16, WORKING DRAFT LOCUS AC019122 SEQUENCE, 12 unordered pieces.

ACCESSION AC019122 VERSION AC019122.3 GI:8318560 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT. SOURCE Homo Sapiens (human)

ORGANISM Homo sapiens

REFERENCE Matarza; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS 1 (bases 1 to 207636)

TITLE The sequence of Homo sapiens clone

JOURNAL Unpublished

REFERENCE Waterston, R.H.

AUTHORS

TITLE Direct Submission

JOURNAL Submitted (30-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108 USA

COMMENT On Jun 7, 2000 this sequence version replaced gi:7109639.

Qry 181 GAGAGAGGTCTGGTCAAGGAGGAGGCTCACAGCTCAGCCCTTGTAC 126355 Db 126294 ATGCTACTCCTCCCTCCACTGCTCTGGTCAAGGAGGAGGCTCACAGCTCAGCCCTTGTAC 126235 Qry 61 CCTCTAGGGCTCTGGATTGCTGCTGTTAACAGAATCTGAGGAGGAGGCTCACAGCTCAGCCCTTGTAC 126295 Db 126354 CCTCTAGGGCTCTGGATTGCTGCTGTTAACAGAATCTGAGGAGGAGGCTCACAGCTCAGCCCTTGTAC 126295 Qry 121 ATGCTACTCCTCCCTCCACTGCTCTGGTCAAGGAGGAGGCTCACAGCTCAGCCCTTGTAC 126355 Db 126234 GAGAGAGCTTGCTGGTCAAGGAGGAGGAGGCTCACAGCTCAGCCCTTGTAC 126175 Qry 241 GAGAGAGCTTGCTGGTCAAGGAGGAGGAGGCTCACAGCTCAGCCCTTGTAC 300 Db 126174 GAGAGAGCTTGCTGGTCAAGGAGGAGGAGGCTCACAGCTCAGCCCTTGTAC 126115

QY	129	TCTGCCTTCCACCTGCCCAGGTGTTAACGGCTGCTCTGGCCCTCTTGCGAGAGAT	188
DB	60543	gap of 100 bp	*
DB	60644	contig of 1666 bp in length	*
DB	62330	gap of 100 bp	*
DB	62429	contig of 1640 bp in length	*
DB	64070	gap of 100 bp	*
DB	64170	contig of 2206 bp in length	*
DB	66375	gap of 100 bp	*
DB	66476	contig of 2497 bp in length	*
DB	68973	gap of 100 bp	*
DB	69073	contig of 1556 bp in length	*
DB	70628	gap of 100 bp	*
DB	70729	contig of 2707 bp in length	*
DB	73435	gap of 100 bp	*
DB	73535	contig of 2236 bp in length	*
DB	75771	contig of 100 bp	*
DB	75772	contig of 2305 bp in length	*
DB	78276	gap of 100 bp	*
DB	78277	contig of 1868 bp in length	*
DB	80145	gap of 100 bp	*
DB	80244	contig of 2119 bp in length	*
DB	82364	gap of 100 bp	*
DB	82463	contig of 1763 bp in length	*
DB	84227	gap of 100 bp	*
DB	84327	contig of 3105 bp in length	*
DB	87432	gap of 100 bp	*
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DB	90277	gap of 100 bp	*
DB	90376	contig of 2647 bp in length	*
DB	93023	gap of 100 bp	*
DB	93123	contig of 2708 bp in length	*
DB	93124	gap of 100 bp	*
DB	95832	contig of 3080 bp in length	*
DB	95932	gap of 100 bp	*
DB	99012	contig of 2611 bp in length	*
DB	99112	gap of 100 bp	*
DB	101722	contig of 3212 bp in length	*
DB	101823	gap of 100 bp	*
DB	105034	contig of 3201 bp in length	*
DB	105135	contig of 2979 bp in length	*
DB	108114	gap of 100 bp	*
DB	112015	contig of 3892 bp in length	*
DB	112106	gap of 100 bp	*
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DB	115407	gap of 100 bp	*
DB	115507	contig of 4208 bp in length	*
DB	119715	gap of 100 bp	*
DB	119814	contig of 5344 bp in length	*
DB	122258	gap of 100 bp	*
DB	125259	contig of 497 bp in length	*
DB	130256	gap of 100 bp	*
DB	130356	contig of 5308 bp in length	*
DB	135664	gap of 100 bp	*
DB	135764	contig of 5582 bp in length	*
DB	141345	gap of 100 bp	*
DB	141446	contig of 4936 bp in length	*
DB	146382	gap of 100 bp	*
DB	146482	contig of 8560 bp in length	*
DB	15042	gap of 100 bp	*
DB	155141	contig of 9229 bp in length	*
DB	164370	gap of 100 bp	*
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DB	164471	gap of 100 bp	*
FEATURES	Location/Qualifiers		
Query Match	99.1%; Score 899; DB 2; Length 164959;		
Best Local Similarity	100.0%; Pred. No. 2e-242;		
Matches	899; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	9 AGGTCGCCAAGCAGCTGCTGAGGCCCAAGGAAGTGGTCAACCTGGACCCCTAGGG	68	
Db	41742 AGGTCCCAAGCAGCTGCTGAGGCCCAAGGAAGTGGTCAACCTGGACCCCTAGGG	41683	
QY	69 GTCTGAGATTCTCTGTCTGAGCTAACCTGAGCCAGGCCCTAGGGAGTGTAC	128	
Db	41682 GTCTGAGATTCTCTGTCTGAGCTAACCTGAGCCAGGCCCTAGGGAGTGTAC	41623	
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	DEFINITION		
	ACCESSION AR129215		
	VERSION AR129215.1		
	KEYWORDS		
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	ORGANISM	Unclassified.	
	REFERENCE	1 (bases 1 to 500)	
	AUTHORS	Bandman, O., Lal, P., Hillman, J. L., Yue, H., Reddy, R., Guebler, K. J. and Baughn, M. R.	
	TITLE	Composition for the detection of genes encoding receptors and proteins associated with cell proliferation	
	JOURNAL	Patent: US 6183968-A 73 06-FEB-2001;	
	FEATURES	Location/Qualifiers	
	Source	1..500	
	Organism	= "unknown"	

ORIGIN /mol_type="unassigned DNA"

Db 480 ATAGGSGATGCTACTCTCCCTCCTCACCTGCTGTGTTACGGTGCCTGCTCC 421

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Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 173 TCTTSCGGAGAGAGTGTCCTCGGGTAGGAAGAGAGGCTCAAGCTCCCT 232

Db 420 TCTTSCGGAGAGAGTGTCCTCGGGTAGGAAGAGAGGCTCAAGCTCCCT 361

Query Match 13.7%; Score 193; DB 6; Length 196;

Best Local Similarity 99.5%; Pred. No. 1.6e-102; Mismatches 0; Indels 0; Gaps 2;

Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 2;

Oy 233 TGTGTTACGGAGAGAGTGTCCTCGGGTAGGAAGAGAGGCTCAAGCTCCCT 292

Db 360 TGTGTTACGGAGAGAGTGTCCTCGGGTAGGAAGAGAGGCTCAAGCTCCCT 301

Query Match 1.97%; Score 196; DB 6; Length 60;

Best Local Similarity 99.5%; Pred. No. 5e-118; Mismatches 0; Indels 2; Gaps 2;

Matches 480; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Oy 293 GCGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 352

Db 300 GCGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 241

Query Match 1.97%; Score 256; DB 6; Length 256;

Best Local Similarity 99.5%; Pred. No. 1.6e-102; Mismatches 0; Indels 0; Gaps 0;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 257 AGSTCCAGGAGGAGTCCCGAGGAGCTCACAGCTCACAGCTCACAGCTCACAGCT 120

Db 121 AGSTCCAGGAGGAGTCCCGAGGAGCTCACAGCTCACAGCTCACAGCTCACAGCT 180

Query Match 1.97%; Score 256; DB 6; Length 256;

Best Local Similarity 99.5%; Pred. No. 1.6e-102; Mismatches 0; Indels 0; Gaps 0;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 317 TCTGTTGCTGTGTTGCGAGCTAACGAGGCTTGGCCAGTCAGCTGGGCGGSCAA 376

Db 181 TCTGTTGCTGTGTTGCGAGCTAACGAGGCTTGGCCAGTCAGCTGGGCGGCAA 240

Query Match 1.97%; Score 376; DB 6; Length 376;

Best Local Similarity 99.5%; Pred. No. 1.6e-102; Mismatches 0; Indels 0; Gaps 0;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 377 ATTCATTAAGAAGCAGAGGGCTGGGCCCCACGAGCTCATTAAGAACACAGGGCTG 436

Db 241 ATTCATTAAGAAGCAGAGGGCTGGGCCCCACGAGCTCATTAAGAACACAGGGCTG 300

Query Match 1.97%; Score 376; DB 6; Length 376;

Best Local Similarity 99.5%; Pred. No. 1.6e-102; Mismatches 0; Indels 0; Gaps 0;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 437 GCTGCTGCCAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGG 496

Db 301 GCTGCTGCCAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGG 350

Query Match 1.97%; Score 496; DB 6; Length 496;

Best Local Similarity 99.5%; Pred. No. 1.6e-102; Mismatches 0; Indels 0; Gaps 0;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 497 ATTGCGCTGGCCGGCCATGTCCTGCTGGAGCTGGAGCTGGAGCTGGAGCTGG 556

Db 361 ATTGCGCTGGCCGGCCATGTCCTGCTGGAGCTGGAGCTGGAGCTGGAGCTGG 420

Query Match 1.97%; Score 556; DB 6; Length 556;

Best Local Similarity 99.5%; Pred. No. 1.6e-102; Mismatches 0; Indels 0; Gaps 0;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 557 GACCCCAAGAGCTTATTGATCTATTGATTTACCACTATTAGCAATTAACTGAG 616

Db 421 GACCCCAAGAGCTTATTGATCTATTGATTTACCACTATTAGCAATTAACTGAG 480

Query Match 1.97%; Score 616; DB 6; Length 616;

Best Local Similarity 99.5%; Pred. No. 1.6e-102; Mismatches 0; Indels 0; Gaps 0;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 481 AATGGGCGCGGCGACGGCTGG 500

RESULT 11
CQ462746/c

LOCUS CQ462746 Sequence 480 bp DNA LINEAR PAT 30-JAN-2004
DEFINITION CO462746 from Patent WO0192581.
ACCESSION CO460389
VERSION CO460389
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE 1. Algate, P.A., Harlocker, S.L. and Jones, R.
AUTHORS Compositions and methods for the therapy and diagnosis of
TITLE ovarian cancer
JOURNAL Patent: WO 0192581-A 3167 06-DEC-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
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Best Local Similarity 99.5%; Pred. No. 1.6e-102; Mismatches 0; Indels 2; Gaps 2;
Matches 425; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Oy 168 GRCCTCTCTGGCGAGAGAGTGTCCTGGTAGGGAGCAGAGGGCTCACAGCTCA 227

Db 425 GRCCTCTCTGGCGAGAGAGTGTCCTGGTAGGGAGCAGAGGGCTCACAGCTCA 366

Query Match 50.5%; Score 458; DB 6; Length 480;

Best Local Similarity 99.6%; Pred. No. 5e-118; Mismatches 0; Indels 2; Gaps 2;

Matches 480; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Oy 228 GCCTTGTACCGAGAGACTGGCCAGGTCCAGTGTCGGAGTCACACACA 287

Db 365 GCCTTGTACCGAGAGACTGGCCAGTGTCGGAGTCACACACA 306

Query Match 50.5%; Score 458; DB 6; Length 480;

Best Local Similarity 99.6%; Pred. No. 5e-118; Mismatches 0; Indels 2; Gaps 2;

Matches 480; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Oy 288 GACTGGCGAGGGAGGGAGCAGTGTCGGAGTCACACACA 347

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Qy	348	CTTGCCGCACTCAGGGTGGGGGGGGAACTCCATAAGAACCCAGAGGTCTGGGCC	407	Qy	550	CTCTCAGGACCCCAGAACAGCTTCATGTGATCTATGATTTAC	594
Db	245	CTTGCCGCACTCAGGGTGGGGGGGGAACTCCATAAGAACCCAGAGGTCTGGGCC	187	Db	45	CTCTCAGGACCCCAGAACGCTTCATGTGATCTATGATTTAC	1
Qy	408	GCGCACAGAGTCATCTGCCAGGAGCTCTGCTGCTGGCAGGGAGGGAGGG	467	RESULT 14	C0463335/c	C0463335	360 bp DNA linear PAT 30-JAN-2004
Db	186	GCGCACAGAGTCATCTGCCAGGAGCTCTGCTGCTGGCAGGGAGGGAGGG	127	LOCUS	Sequence 6113 from Patent WO01192581.		
Qy	468	GCGTGTGGCCAGTAAGAACCAAGGGGATTCGGCATGTCCTGGCTAGG	527	DEFINITION	Sequence 6113 from Patent WO01192581.		
Db	126	GCGTGTGGCCAGTAAGAACCAAGGGGATTCGGCATGTCCTGGCTAGG	68	ACCESSION	C0463335		
Qy	528	GCGCACAGTCACCTTGTGCTGGAGGCCAAGAGCTTCATGTATATGA	587	VERSION	C0463335.1. GI:41428954		
Db	67	GCGCACAGTCACCTTGTGCTGGAGGCCAAGAGCTTCATGTATATGA	8	KWORDS			
Qy	588	TTTTAC 594		ORGANISM	Homo sapiens (human)		
Db	7	TTTTAC 1		REFERENCE	Bukayto, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
				AUTHORS	Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.		
				TITLE	Algate, P.A., Harlocker, S.L. and Jones, R. Compositions and methods for the therapy and diagnosis of ovariancancer		
				JOURNAL	Patent: WO 0122581-A 6113 06-DEC-2001; CORIXA CORPORATION (US)		
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					360 TGTATCCTGAGGACACTGGCAAGGATGGTCCACACAGACTGG	301	
					294 CGCGAGGCGAGGGGCGACAGTCTGTGCTTGGTTGACAGTAAGAGGGCTCTGGC	353	
					300 CGCGAGGCGAGGGGCGACAGTCTGTGCTTGGTTGACAGTAAGAGGGCTCTGGC	241	
					354 CAGTCAGGTTGGGGCAACTCTATAGAACAGAGGCTCTGGGGCGGCGAC	413	
					Db 240 CAGTCAGGTTGGGGCGGCAACTCTATAGAACAGAGGCTCTGGGGCGAC	182	
					414 AGAGTCATCTGCCAGCTCTCGCTGCTGGCAGTGGAGGGCTCTGGGGCTT	473	
					181 AGAGTCATCTGCCAGCTCTCGCTGCTGGCAGTGGAGGGCTT	122	
					474 GTGCGAGTAAACACAGCTGATTCCTCGCTGGCAGTGGAGGGCTCTGGAGGAC	533	
					Db 121 GTGCGAGTAAACACAGCTGATTCCTCGCTGGCAGTGGAGGGCTT	62	
					534 ATTCTCAACCTCTGCTCTAGACGCCAAGAGCTTCATGTATATGATT	593	
					Db 61 ATTCTCAACCTCTGCTCTAGACGCCAAGAGCTTCATGTATATGATT	2	
					Qy 594 C 594		
					Db 1 C 1		
				RESULT 15			
				AX071596	AX071596	399 bp DNA linear PAT 25-JAN-2001	
				LOCUS	Sequence 2068 from Patent WO0102568.		
				DEFINITION			
				ACCESSION	AX071596		
				VERSION	AX071596.1. GI:12581947		
				KWORDS			
				SOURCE	Homo sapiens (human)		

ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Williams L.T., Escobedo J., Innis M.A., Garcia P.D., Klinger J.,
 Kasam A., Reinhard C., Randazzo F., Kennedy G.C., Per D.,
 Lamont G., Drmanac R., Turkmenakov R., Drmanac S., Dickson M.,
 Labat I., Leskowitiz D., Kita D., Garcia V. and Strachan-Crain B.

TITLE Human genes and gene expression products

JOURNAL Patent: WO 012568-A 2008 11-JAN-2001;

CHIRON CORPORATION (US); HYSEQ, INC. (US)

FEATURES Location/Qualifiers

Source

1. .399
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 24.6%; Score 222.8; DB 6; Length 399;
 Best Local Similarity 99.1%; Pred. No. 1 2e-51; Mismatches 0; Gaps 0;
 Matches 224; Conservative 0; Indels 2;

Qy	1	GACTCTGAGGCCAGCAGCAGCTGCTGAGGCCAGGAGTGCTCCACCTTGAC	60
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Qy	61	CCTCTAGGGTCTGGATTGCTGTAACTGAAGTAACCTGAGSGCAGCCATAGGAA	120
Db	234	CCTCTAGGGTCTGGATTGCTGTAACTGAAGTAACCTGAGGCAGGACCCATAGGAA	293
Qy	121	ATGCTTACCTCCCTCCCTTCACCACTGGCTGGTTCAGGGCGCTGGTCCCTTGCC	180
Db	294	ATGCTTACCTCCCTCCCTTCACCACTGGCTGGTTCAGGGCGCTGGTCCCTTGCC	353
Qy	181	GAGAGAGTGCTCTGGGAGGAGCAGAGAGCTCACAGACTCC	226
Db	354	GAGAGAGTGCTCTGGGAGGAGCAGAGAGCTCACAGACTCC	399

Search completed: September 15, 2005, 17:07:39
 Job time : 4546 secs

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OM nucleic - nucleic search, using sw model
 Run on: September 15, 2005, 19:53:12 ; Search time 775 Seconds
 (without alignment)
 7797.358 Million cell updates/sec

Perfect score: 907
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Total number of hits satisfying chosen parameters: 14778644
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Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Database :

Published Applications_NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
27	907	100.0	907 10 US-00-997-428-398	Sequence 398, App
119	907	100.0	907 15 US-10-219-065-97	Sequence 97, App
177	907	100.0	907 22 US-10-950-374-998	Sequence 398, App
178	907	100.0	17761 9 US-09-764-847-1596	Sequence 956, App
179	907	100.0	17761 14 US-10-092-154-1596	Sequence 1596, App
180	601.6	66.3	1154 18 US-10-302-172-204	Sequence 204, App
C 181	458	50.5	480 9 US-09-867-701-524	Sequence 5524, App
C 182	403	44.4	425 9 US-09-867-701-3167	Sequence 3167, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

c	256	206.2	22.7	48336	9	US-09-927-602-38	Sequence 38, Appli	c	329	204	22.5	33137	17	US-10-292-798-913	
c	257	206	22.7	11486	20	US-09-417-715-18	Sequence 18, Appli	c	330	204	22.5	48841	10	US-09-844-653-32	
c	258	205.8	22.7	93420	13	US-10-087-192-46	Sequence 46, Appli	c	331	204	22.5	56348	10	US-10-741-560-536	
c	259	205.8	22.7	59554	18	US-10-052-482-202	Sequence 202, Appli	c	332	203.8	22.5	717	13	US-10-027-632-130796	
c	260	205.8	22.7	20354	9	US-09-820-905-3	Sequence 3, Appli	c	333	203.8	22.5	717	13	US-10-027-632-130796	
c	261	205.8	22.7	20354	22	US-10-473-338A-3	Sequence 3, Appli	c	334	203.8	22.5	892	13	US-10-027-632-130796	
c	262	205.8	22.7	260549	21	US-10-741-600-17723	Sequence 17723, A	c	335	203.8	22.5	892	17	US-10-027-632-164445	
c	263	205.6	22.7	10085	10	US-09-764-891-5491	Sequence 5491, AP	c	336	203.8	22.5	3635	18	US-10-344-394-43	
c	264	205.6	22.7	142519	22	US-10-479-874A-9	Sequence 9, Appli	c	337	203.8	22.5	8735	18	US-10-344-394-41	
c	265	205.4	22.6	710	13	US-10-027-632-110510	Sequence 110510, A	c	338	203.8	22.5	16640	19	US-10-741-601-5666	
c	266	205.4	22.6	710	17	US-10-027-632-110510	Sequence 110510,	c	339	203.8	22.5	16640	21	US-10-741-600-17696	
c	267	205.4	22.6	860	13	US-10-027-632-130797	Sequence 130797,	c	340	203.8	22.5	18235	19	US-10-741-601-5717	
c	268	205.4	22.6	860	17	US-10-027-632-130797	Sequence 130797,	c	341	203.8	22.5	18235	21	US-10-741-600-17831	
c	269	205.4	22.6	2619	19	US-10-363-829-250	Sequence 250, APP	c	342	203.8	22.5	53413	17	US-10-052-482-220	
c	270	205.4	22.6	56316	9	US-09-901-482A-1	Sequence 1, Appli	c	343	203.8	22.5	60461	17	US-10-344-434-82	
c	271	205.4	22.6	56316	9	US-09-853-528-1	Sequence 1, Appli	c	344	203.4	22.4	888	13	US-10-072-632-121467	
c	272	205.4	22.6	56320	9	US-09-553-526-179	Sequence 179, APP	c	345	203.4	22.4	4067	10	US-10-741-601-5717	
c	273	205.4	22.6	67253	22	US-10-737-082-88	Sequence 179, APP	c	346	203.4	22.4	4067	10	US-09-764-891-7225	
c	274	205.4	22.6	67253	22	US-10-765-790-88	Sequence 179, APP	c	347	203.4	22.4	4067	10	US-09-764-887-338	
c	275	205.4	22.6	67253	22	US-10-997-722-154	Sequence 1, Appli	c	348	203.4	22.4	32190	14	US-10-071-961-338	
c	276	205.4	22.6	96594	11	US-10-997-722-154	Sequence 1, Appli	c	349	203.4	22.4	56737	9	US-09-782-378A-17	
c	277	205.4	22.6	150525	22	US-10-981-277-36	Sequence 3, Appli	c	350	203.4	22.4	22.4	22.4	Sequence 12467, AP	
c	278	205.4	22.6	168336	22	US-10-981-277-35	Sequence 3, Appli	c	351	203.4	22.4	22.4	19335	18	US-10-235-192A-45
c	279	205.4	22.6	17091	15	US-10-553-34-2	Sequence 1, Appli	c	352	203.4	22.4	21	18	US-10-461-862-98	
c	280	205.2	22.6	1098	13	US-10-027-632-10720	Sequence 10720, A	c	353	203.2	22.4	49083	13	US-10-071-192-826	
c	281	205.2	22.6	1098	17	US-10-027-632-10720	Sequence 10720, A	c	354	203.2	22.4	256190	9	US-10-322-281-320	
c	282	205.2	22.6	3660	22	US-10-514-744-42	Sequence 42, Appli	c	360	203	22.4	22.4	32190	14	US-10-022-632-102138
c	283	205.2	22.6	3673	22	US-10-511-744-3	Sequence 3, Appli	c	361	203	22.4	22.4	32190	14	US-10-022-632-102138
c	284	205.2	22.6	3673	22	US-10-514-744-9	Sequence 9, Appli	c	362	203	22.4	22.4	32190	14	US-10-022-632-102138
c	285	205.2	22.6	3674	22	US-10-514-744-11	Sequence 11, Appli	c	363	203	22.4	22.4	32190	14	US-10-022-632-102138
c	286	205.2	22.6	3675	22	US-10-514-744-7	Sequence 11, Appli	c	364	203	22.4	22.4	32190	14	US-10-022-632-102138
c	287	205.2	22.6	3702	22	US-10-514-744-5	Sequence 11, Appli	c	365	202.8	22.4	22.4	32190	14	US-10-022-632-102138
c	288	205.2	22.6	3702	22	US-10-514-744-5	Sequence 11, Appli	c	366	202.8	22.4	22.4	32190	14	US-10-022-632-102138
c	289	205.2	22.6	51001	17	US-10-741-600-1809	Sequence 18005, A	c	367	202.8	22.4	22.4	32190	14	US-10-022-632-102138
c	290	205.2	22.6	51001	21	US-10-292-798-1789	Sequence 1789, A	c	368	202.8	22.4	22.4	32190	14	US-10-022-632-102138
c	291	205.2	22.6	18303	21	US-10-741-600-17807	Sequence 11, Appli	c	369	202.8	22.4	22.4	32190	14	US-10-022-632-102138
c	292	205.2	22.6	51001	17	US-10-189-268-11	Sequence 11, Appli	c	370	202.8	22.4	22.4	32190	14	US-10-022-632-102138
c	293	204.8	22.6	22768	20	US-10-012-800-1357	Sequence 1357, AP	c	371	202.8	22.4	22.4	32190	14	US-10-022-632-102138
c	294	204.8	22.6	2289	14	US-10-115-282-3	Sequence 3, Appli	c	372	202.8	22.4	22.4	32190	14	US-10-022-632-102138
c	295	204.8	22.6	2289	20	US-10-762-966-3	Sequence 1759, A	c	373	202.8	22.4	22.4	32190	14	US-10-022-632-102138
c	296	204.8	22.6	2289	20	US-10-762-966-3	Sequence 1759, A	c	374	202.8	22.4	22.4	32190	14	US-10-022-632-102138
c	297	204.8	22.6	2289	21	US-10-762-966-3	Sequence 1759, A	c	375	202.8	22.4	22.4	32190	14	US-10-022-632-102138
c	298	204.8	22.6	2289	21	US-10-762-966-3	Sequence 1759, A	c	376	202.8	22.4	22.4	32190	14	US-10-022-632-102138
c	299	204.8	22.6	16849	17	US-10-085-117-250	Sequence 2143, AP	c	377	202.8	22.4	22.4	32190	14	US-10-098-880-107-428
c	300	204.8	22.6	16849	17	US-10-085-117-250	Sequence 250, APP	c	378	202.8	22.4	22.4	32190	14	US-10-098-880-107-428
c	301	204.6	22.6	95689	17	US-10-085-117-130	Sequence 1, Appli	c	379	202.8	22.4	22.4	32190	14	US-10-098-880-107-428
c	302	204.6	22.6	122014	13	US-10-087-192-1726	Sequence 130, APP	c	380	202.8	22.4	22.4	32190	14	US-10-098-880-107-428
c	303	204.6	22.6	24782	18	US-10-235-192A-28	Sequence 1726, AP	c	381	202.6	22.3	22.3	32190	14	US-10-098-880-107-428
c	304	204.4	22.5	14117	9	US-09-850-670-251	Sequence 28, Appli	c	382	202.6	22.3	22.3	32190	14	US-10-098-880-107-428
c	305	204.4	22.5	14117	17	US-10-227-666-251	Sequence 251, APP	c	383	202.6	22.3	22.3	32190	14	US-10-098-880-107-428
c	306	204.4	22.5	14216	9	US-09-850-670-249	Sequence 1, Appli	c	384	202.6	22.3	22.3	32190	14	US-10-098-880-107-428
c	307	204.4	22.5	14216	17	US-10-227-666-249	Sequence 249, APP	c	385	202.6	22.3	22.3	32190	14	US-10-098-880-107-428
c	308	204.4	22.5	20538	21	US-10-741-600-17954	Sequence 1759, A	c	386	202.6	22.3	22.3	32190	14	US-10-098-880-107-428
c	309	204.4	22.5	23979	21	US-10-741-600-17628	Sequence 17626, A	c	387	202.4	22.3	22.3	32190	14	US-10-098-880-107-428
c	310	204.4	22.5	167163	17	US-10-394-48-31	Sequence 31, Appli	c	388	202.4	22.3	22.3	32190	14	US-10-098-880-107-428
c	311	204.4	22.5	47336	17	US-10-452-510-15	Sequence 15, Appli	c	389	202.4	22.3	22.3	32190	14	US-10-098-880-107-428
c	312	204.2	22.5	47336	18	US-10-617-334-15	Sequence 15, Appli	c	390	202.4	22.3	22.3	32190	14	US-10-098-880-107-428
c	313	204.2	22.5	47336	19	US-10-744-665-15	Sequence 15, Appli	c	391	202.4	22.3	22.3	32190	14	US-10-098-880-107-428
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c	316	204.2	22.5	11754	10	US-09-984-827-5	Sequence 5, Appli	c	394	202.4	22.3	22.3	32190	14	US-10-098-880-107-428
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c	319	204.2	22.5	15572	22	US-10-981-877-30	Sequence 5, Appli	c	397	202.4	22.3	22.3	32190	14	US-10-098-880-107-428
c	320	204.2	22.5	159338	20	US-10-719-993-6777	Sequence 6777, AP	c	398	202.4	22.3	22.3	32190	14	US-10-098-880-107-428
c	321	204.2	22.5	159338	21	US-10-718-219-15	Sequence 17613, A	c	399	202.4	22.3	22.3	32190	14	US-10-098-880-107-428
c	322	204.2	22.5	183999	19	US-10-745-377-1	Sequence 1, Appli	c	400	202.4	22.3	22.3	32190</		

C 402	202.2	22.3	850	17	US-10-027-632-30982	Sequence 30982, A	475	201.6	22.2	8896	17	US-10-074-024-666
C 403	202.2	22.3	1158	13	US-10-027-632-122621	Sequence 122621, A	C 476	201.6	22.2	12430	16	US-10-300-453A-26
C 404	202.2	22.3	1158	13	US-10-027-632-122622	Sequence 122622, A	C 477	201.6	22.2	14405	16	US-10-300-453A-27
C 405	202.2	22.3	1158	13	US-10-027-632-122623	Sequence 122623, A	C 478	201.6	22.2	17758	17	US-10-264-237-2833
C 406	202.2	22.3	1158	17	US-10-027-632-122621	Sequence 122621, A	C 479	201.6	22.2	32134	17	US-10-242-355-316
C 407	202.2	22.3	1158	17	US-10-027-632-122622	Sequence 122622, A	C 480	201.6	22.2	50602	13	US-10-087-192-448
C 408	202.2	22.3	1158	17	US-10-027-632-122623	Sequence 122623, A	C 481	201.6	22.2	73764	19	US-10-741-601-5616
C 409	202.2	22.3	1159	13	US-10-027-632-124039	Sequence 124039, A	C 482	201.6	22.2	235033	15	US-10-301-844-1
C 410	202.2	22.3	1159	13	US-10-027-632-124040	Sequence 124040, A	C 483	201.6	22.2	237326	15	US-10-301-844-2
C 411	202.2	22.3	1369	13	US-10-027-632-124038	Sequence 124038, A	C 484	201.6	22.2	406	10	US-09-918-995-8791
C 412	202.2	22.3	1369	17	US-10-027-632-124039	Sequence 124039, A	C 485	201.6	22.2	11722	10	US-09-855-612-1
C 413	202.2	22.3	1369	17	US-10-027-632-124040	Sequence 124040, A	C 486	201.6	22.2	15783	10	US-09-764-872-700
C 414	202.2	22.3	9365	13	US-10-091-085-8	Sequence 8, AppI	C 488	201.6	22.2	28953	20	US-10-719-993-8811
C 415	202.2	22.3	9365	13	US-10-032-065-8	Sequence 8, AppI	C 489	201.6	22.2	42954	13	US-10-087-192-934
C 416	202.2	22.3	9165	16	US-10-286-926-42	Sequence 42, AppI	C 490	201.6	22.2	59856	13	US-10-087-192-964
C 417	202.2	22.3	14747	16	US-10-286-926-42	Sequence 17736, A	C 491	201.6	22.2	44667	14	US-10-274-409-3
C 418	202.2	22.3	23886	21	US-10-741-600-17736	Sequence 802, AppI	C 492	201.6	22.2	64647	21	US-10-932-135-3
C 419	202.2	22.3	502	10	US-09-918-995-13187	Sequence 1927, A	C 493	201.6	22.2	64685	21	US-10-741-600-17984
C 420	202.2	22.3	56510	21	US-10-741-600-17637	Sequence 17637, A	C 494	201.6	22.2	56885	21	US-10-741-600-17643
C 421	202.2	22.3	99014	9	US-09-880-110-73420	Sequence 3428, AppI	C 495	201.6	22.2	118356	21	US-09-962-436-281
C 422	202.2	22.3	109516	13	US-10-037-192-220	Sequence 220, AppI	C 496	201.6	22.2	167343	9	US-09-964-844A-273
C 423	202.2	22.3	124990	20	US-10-684-422-156	Sequence 156, AppI	C 497	201.6	22.2	167343	21	US-10-087-192-964
C 424	202.2	22.3	172049	22	US-10-56-142-2157	Sequence 2157, AppI	C 498	201.6	22.2	167343	21	US-10-087-192-964
C 425	202.2	22.3	23886	21	US-10-027-633-28555	Sequence 13187, A	C 499	201.6	22.2	167343	21	US-10-932-135-3
C 426	202	22.3	502	10	US-10-027-633-28555	Sequence 28535, A	C 500	201.6	22.2	337344	19	US-10-388-838-58
C 427	202	22.3	760	13	US-10-027-632-13514	Sequence 13514, A	C 501	201.6	22.2	626	13	US-10-027-632-13331
C 428	202	22.3	760	13	US-10-027-633-28558	Sequence 144959, A	C 502	201.6	22.2	626	17	US-10-027-632-13331
C 429	202	22.3	760	17	US-10-027-633-28559	Sequence 144958, A	C 503	201.6	22.2	637	13	US-10-027-632-288478
C 430	202	22.3	760	17	US-10-027-632-144958	Sequence 28535, A	C 504	201.6	22.2	637	17	US-10-027-632-288478
C 431	202	22.3	852	13	US-10-027-633-28555	Sequence 28536, A	C 505	201.6	22.2	1557	20	US-10-723-860-2009
C 432	202	22.3	852	17	US-10-027-632-28535	Sequence 28535, A	C 506	201.6	22.2	1557	22	US-10-756-149-889
C 433	202	22.3	852	17	US-10-027-632-28535	Sequence 28536, A	C 507	201.6	22.2	1557	22	US-10-756-149-889
C 434	202	22.3	852	17	US-10-027-633-28536	Sequence 1655, AppI	C 508	201.6	22.2	1837	13	US-10-027-632-289405
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C 436	202	22.3	2446	13	US-10-027-633-101879	Sequence 101879, AppI	C 510	201.6	22.2	1837	17	US-10-027-632-289405
C 437	202	22.3	2680	13	US-10-027-633-11718	Sequence 111718, AppI	C 511	201.6	22.2	14426	9	US-09-860-670-252
C 438	202	22.3	2680	17	US-10-027-632-11718	Sequence 111718, AppI	C 512	201.6	22.2	14426	17	US-10-227-646-252
C 439	202	22.3	2680	17	US-10-461-862-98	Sequence 589, AppI	C 513	201.6	22.2	14426	17	US-10-632-249404
C 440	202	22.3	2738417	21	US-10-461-862-98	Sequence 589, AppI	C 514	201.6	22.2	227426	19	US-10-085-117-256
C 441	202	22.3	271751	20	US-10-719-933-6817	Sequence 6817, AppI	C 515	201.6	22.2	227426	19	US-10-085-117-256
C 442	202	22.3	32433	18	US-10-027-632-136	Sequence 136, AppI	C 516	201.6	22.2	227426	19	US-10-027-632-276891
C 443	202	22.3	44466	20	US-10-719-933-6884	Sequence 6884, AppI	C 517	201.6	22.2	227426	19	US-10-027-632-276891
C 444	202	22.3	6952	19	US-10-322-81-72	Sequence 72, AppI	C 518	201.6	22.2	227426	19	US-10-322-81-72
C 445	202	22.3	86893	21	US-10-711-60-17773	Sequence 1773, AppI	C 519	201.6	22.2	227426	19	US-10-618-941-11
C 446	202	22.3	956	13	US-10-027-632-17700	Sequence 98, AppI	C 520	201.6	22.2	227426	19	US-10-618-941-11
C 447	202	22.3	956	17	US-10-027-632-187700	Sequence 187100, AppI	C 521	201.6	22.2	227426	19	US-10-618-941-11
C 448	202	22.3	11891	9	US-09-764-877-2942	Sequence 2942, AppI	C 522	201.6	22.2	227426	19	US-10-618-941-11
C 449	202	22.3	1980090	21	US-09-10-027-641-600-17676	Sequence 17676, A	C 523	201.6	22.2	3404	19	US-10-322-281-25
C 450	201.8	22.2	6952	13	US-10-027-632-187700	Sequence 187099, AppI	C 524	201.6	22.2	3404	19	US-10-618-941-11
C 451	201.8	22.2	86893	21	US-10-711-60-17773	Sequence 187100, AppI	C 525	201.6	22.2	3404	19	US-10-618-941-11
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C 453	201.8	22.2	956	17	US-10-027-633-187700	Sequence 187100, AppI	C 527	201.6	22.2	3404	19	US-10-618-941-11
C 454	201.8	22.2	11891	9	US-09-764-877-2942	Sequence 2942, AppI	C 528	201.6	22.2	3404	19	US-10-618-941-11
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C 459	201.8	22.2	100762	19	US-10-322-696-154	Sequence 11, AppI	C 533	201.6	22.2	3404	19	US-10-618-941-11
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C 461	201.8	22.2	161531	19	US-10-322-281-252	Sequence 8993, AppI	C 535	201.6	22.2	3404	19	US-10-618-941-11
C 462	201.8	22.2	175077	13	US-10-087-192-1168	Sequence 1168, AppI	C 536	201.6	22.2	3404	19	US-10-618-941-11
C 463	201.8	22.2	193357	17	US-10-085-17-142	Sequence 142, AppI	C 537	201.6	22.2	3404	19	US-10-618-941-11
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C 467	201.8	22.2	379652	21	US-10-481-613-71	Sequence 71, AppI	C 541	200.8	22.1	3404	19	US-10-618-941-11
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C 471	201.6	22.2	839	17	US-10-027-632-169015	Sequence 169015, AppI	C 545	200.8	22.1	644	13	US-10-027-632-238835
C 472	201.6	22.2	2666	17	US-10-074-024-667	Sequence 667, AppI	C 546	200.8	22.1	644	13	US-10-027-632-102523
C 473	201.6	22.2	8896	9	US-09-764-855-331	Sequence 331, AppI	C 547	200.8	22.1	644	13	US-10-027-632-102523
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553	200.8	22.1	4421	14	US-10-216-373-5	Sequence 6, Appl1	626	200.2	22.1	256157	13	US-10-087-192-1204
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612	200.2	22.1	1032	17	US-10-027-632-116724	Sequence 1, Appli	685	199.8	22.0	27246	19	Sequence 332, App
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C	699	199.6	22.0	1262	17	US-10-027-633-263009	Sequence 263009, Appl
C	700	199.6	22.0	2361	17	US-10-094-749-47	Sequence 47, Appl
C	701	199.6	22.0	3178	13	US-10-027-632-113304	Sequence 113304, Appl
C	702	199.6	22.0	3178	17	US-10-027-633-113304	Sequence 113304, Appl
C	703	199.6	22.0	3262	13	US-10-098-841-83	Sequence 83, Appl
C	704	199.6	22.0	3406	13	US-10-027-632-118334	Sequence 118334, Appl
C	705	199.6	22.0	3406	17	US-10-027-632-118334	Sequence 118334, Appl
C	706	199.6	22.0	3406	21	US-10-433-577-30	Sequence 30, Appl
C	707	199.6	22.0	3716	17	US-10-027-632-113835	Sequence 30, Appl
C	708	199.6	22.0	4037	9	US-09-976-674-40	Sequence 40, Appl
C	709	199.6	22.0	4037	21	US-10-982-512-40	Sequence 40, Appl
C	710	199.6	22.0	4076	9	US-09-976-674-32	Sequence 32, Appl
C	711	199.6	22.0	4076	21	US-10-982-512-32	Sequence 32, Appl
C	712	199.6	22.0	4120	9	US-09-976-674-38	Sequence 38, Appl
C	713	199.6	22.0	4120	21	US-10-982-512-38	Sequence 38, Appl
C	714	199.6	22.0	4159	9	US-09-976-674-30	Sequence 30, Appl
C	715	199.6	22.0	4159	21	US-10-982-512-30	Sequence 30, Appl
C	716	199.6	22.0	4180	9	US-09-976-674-36	Sequence 36, Appl
C	717	199.6	22.0	4180	21	US-10-982-512-36	Sequence 36, Appl
C	718	199.6	22.0	4219	9	US-09-976-674-28	Sequence 28, Appl
C	719	199.6	22.0	4219	21	US-10-982-512-28	Sequence 28, Appl
C	720	199.6	22.0	4263	9	US-09-976-674-34	Sequence 34, Appl
C	721	199.6	22.0	4263	21	US-10-982-512-34	Sequence 34, Appl
C	722	199.6	22.0	4302	9	US-09-976-674-24	Sequence 24, Appl
C	723	199.6	22.0	4302	21	US-09-976-674-24	Sequence 24, Appl
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C	726	199.6	22.0	52745	13	US-10-027-632-218458	Sequence 1456, Ap
C	727	199.6	22.0	616704	13	US-10-087-192-1456	Sequence 34, Ap
C	728	199.6	22.0	135827	19	US-10-322-281-232	Sequence 34, Ap
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C	730	199.6	22.0	142976	21	US-10-367-94-99	Sequence 99, Ap
C	731	199.6	22.0	181698	13	US-10-087-192-790	Sequence 790, Ap
C	732	199.6	22.0	181698	21	US-10-087-192-790	Sequence 790, Ap
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C	736	199.6	22.0	1664	9	US-09-764-877-2841	Sequence 281, Ap
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C	738	199.4	22.0	1756	17	US-10-108-60R-2159	Sequence 2159, Ap
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C	740	199.4	22.0	186196	14	US-10-021-608-132	Sequence 132, Ap
C	741	199.4	22.0	186196	15	US-10-017-161-1579	Sequence 1579, Ap
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843	198.6	21.9	86880	22	US-10-756-159-1653	Sequence 1653, Appl	916	198.2	21.9	32194	10	US-10-764-891-1028	
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857	198.6	21.9	14533	22	US-10-756-149-921	Sequence 921, Appl	930	198.2	21.9	317876	21	US-10-741-601-5629	
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c 886	198.6	21.9	22186	17	US-10-085-117-178	Sequence 178, Appl	959	198.2	21.9	317876	21	US-10-741-600-17607	
c 887	198.6	21.9	22186	17	US-10-085-117-178	Sequence 178, Appl	960	198.2	21.9	317876	21	US-10-741-600-17607	
c 888	198.6	21.9	86081	19	US-10-741-601-5840	Sequence 5640, Appl	961	198.2	21.9	317876	21	US-10-741-600-17607	
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c 891	198.6	21.9	87689	19	US-10-717-597-194	Sequence 194, Appl	964	198.2	21.9	317876	21	US-10-741-600-17607	
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c 895	198.6	21.9	143899	10	US-09-972-546-15	Sequence 15, Appl	968	198.2	21.9	317876	21	US-10-741-600-17607	
c 896	198.6	21.9	143899	21	US-10-556-149-592	Sequence 15, Appl	969	198.2	21.9	317876	21	US-10-741-600-17607	
c 897	198.6	21.9	174424	9	US-09-967-768A-314	Sequence 31, Appl	970	198.2	21.9	317876	21	US-10-741-600-17607	
c 898	198.6	21.9	174424	10	US-09-960-006-969	Sequence 969, Appl	971	198.2	21.9	317876	21	US-10-741-600-17607	
c 899	198.6	21.9	174424	21	US-10-843-414A-6459	Sequence 6459, Appl	972	198.2	21.9	317876	21	US-10-741-600-17607	
c 900	198.6	21.9	181343	20	US-10-723-860-2392	Sequence 2392, Appl	973	198.2	21.9	317876	21	US-10-741-600-17607	
c 901	198.6	21.9	181343	22	US-10-756-149-2215	Sequence 2215, Appl	974	198.2	21.9	317876	21	US-10-741-600-17607	
c 902	198.6	21.9	181343	22	US-10-820-905-3	Sequence 3, Appl	975	198.2	21.9	317876	21	US-10-741-600-17607	
c 903	198.6	21.9	203654	22	US-10-473-338A-3	Sequence 3, Appl	976	198.2	21.9	317876	21	US-10-741-600-17607	
c 904	198.6	21.9	203654	22	US-10-277-632-123226	Sequence 123226, Appl	977	198.2	21.9	317876	21	US-10-741-600-17607	
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c 911	198.6	21.9	1326	17	US-10-108-260-1541	Sequence 123226, Appl	984	198.2	21.9	317876	21	US-10-741-600-176	

C	986	197.8	21.8	648	17	US-10-027-632-107015	1059	197.4	21.8	1449	21	US-10-887-553A-909	
C	987	197.8	21.8	1167	22	US-10-999-333A-2	1060	197.4	21.8	1449	21	US-10-956-157-2117	
C	988	197.8	21.8	3129	9	US-09-735-103-9	1061	197.4	21.8	1599	14	US-10-153-668-139	
C	989	197.8	21.8	3129	13	US-05-438A-9	1062	197.4	21.8	14963	19	US-10-741-601-5776	
C	990	197.8	21.8	3105	10	US-09-822-846-279	1063	197.4	21.8	23469	19	US-10-741-601-5599	
C	991	197.8	21.8	6510	13	US-10-098-841-139	1064	197.4	21.8	3175	19	US-10-741-601-5551	
C	992	197.8	21.8	21913	10	US-09-764-891-6065	1065	197.4	21.8	46566	20	US-10-719-693-6510	
C	993	197.8	21.8	21913	10	US-09-764-891-6066	1066	197.4	21.8	45656	21	US-10-741-600-17829	
C	994	197.8	21.8	21913	10	US-09-764-891-6067	1067	197.4	21.8	52710	19	US-10-322-281-572	
C	995	197.8	21.8	1067	17	US-10-187-659A-11	1068	197.4	21.8	61765	19	US-10-322-281-624	
C	996	197.8	21.8	28616	17	US-10-455-552-1	1069	197.4	21.8	63255	13	US-10-087-192-772	
C	997	197.8	21.8	32191	17	US-10-074-044-446	1070	197.4	21.8	117231	22	US-10-893-315-129	
C	998	197.8	21.8	32865	13	US-10-087-192-964	1071	197.4	21.8	17424	9	US-09-967-7608-314	
C	999	197.8	21.8	53522	10	US-09-904-968A-1	1072	197.4	21.8	17424	10	US-09-960-7606-969	
C	1000	197.8	21.8	70542	13	US-10-057-191-1294	1073	197.4	21.8	17424	21	US-10-843-61A-649	
C	1001	197.8	21.8	197	15	US-10-755-163-352	1074	197.4	21.8	181343	20	US-10-723-860-2392	
C	1002	197.8	21.8	98716	21	US-10-741-600-17754	1075	197.4	21.8	181343	22	US-10-755-149-2215	
C	1003	197.8	21.8	103660	21	US-10-741-600-17645	1076	197.4	21.8	187044	20	US-10-719-993-6083	
C	1004	197.8	21.8	113000	16	US-10-766-165-16	1077	197.4	21.8	214000	21	US-10-829-674-1	
C	1005	197.8	21.8	128034	17	US-10-282-174-186	1078	197.4	21.8	214000	21	US-10-830-677-1	
C	1006	197.8	21.8	128034	17	US-10-600-001-186	1079	197.4	21.8	47794	21	US-10-723-670-1	
C	1007	197.8	21.8	186669	13	US-10-087-192-340	1080	197.4	21.8	465237	9	US-09-933-267A-1	
C	1008	197.8	21.8	134292	18	US-10-240-425-1102	1081	197.2	21.7	402	19	US-10-674-124A-386	
C	1009	197.8	21.8	134292	21	US-10-278-698-335	1082	197.2	21.7	600	21	US-10-575-157-772	
C	1010	197.8	21.8	134292	21	US-10-278-698-849	1083	197.2	21.7	648	13	US-10-027-632-112653	
C	1011	197.8	21.8	162450	15	US-10-071-179-1	1084	197.2	21.7	648	13	US-10-027-632-112654	
C	1012	197.8	21.8	162450	16	US-10-156-704-1	1085	197.2	21.7	648	17	US-10-027-632-112653	
C	1013	197.8	21.8	162450	17	US-10-282-174-484	1086	197.2	21.7	658	10	US-09-953-318-20	
C	1014	197.8	21.8	202100	21	US-10-600-009-484	1087	197.2	21.7	751	17	US-10-445-157-772	
C	1015	197.8	21.8	255439	21	US-10-719-93-6799	1088	197.2	21.7	854	13	US-10-027-632-163774	
C	1016	197.8	21.8	300000	15	US-10-252-553-33	1089	197.2	21.7	854	17	US-10-027-632-167774	
C	1017	197.8	21.8	325791	19	US-10-703-210-33	1090	197.2	21.7	902	21	US-10-755-157-7286	
C	1018	197.8	21.8	325791	19	US-10-708-188A-1	1091	197.2	21.7	902	21	US-10-764-881-5709	
C	1019	197.8	21.8	601	9	US-09-819-656-60	1092	197.2	21.7	6658	18	US-10-974-821-8885	
C	1020	197.6	21.8	601	9	US-09-818-656A-62	1093	197.2	21.7	85763	18	US-10-974-821-8885	
C	1021	197.6	21.8	2702	10	US-09-822-848-142	1094	197.2	21.7	33478	19	US-10-322-281-188	
C	1022	197.6	21.8	15286	21	US-10-741-600-17608	1095	197.2	21.7	35804	21	US-10-898-406-3	
C	1023	197.6	21.8	23626	9	US-09-764-878-261	1096	197.2	21.7	40433	9	US-09-800-107-3327	
C	1024	197.6	21.8	23626	9	US-09-764-860-940	1097	197.2	21.7	40433	22	US-10-755-149-155	
C	1025	197.6	21.8	23632	14	US-10-079-854-261	1098	197.2	21.7	57159	22	US-10-783-211-108	
C	1026	197.6	21.8	23632	14	US-10-079-854-261	1099	197.2	21.7	57763	18	US-10-052-402-34	
C	1027	197.6	21.8	23626	17	US-10-212-872-941	1100	197.2	21.7	70000	17	US-10-723-13	
C	1028	197.6	21.8	23632	17	US-10-034-650-58	1101	197.2	21.7	92139	9	US-09-918-686-1	
C	1029	197.6	21.8	23632	19	US-10-689-878-262	1102	197.2	21.7	92139	16	US-10-353-150-1	
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C	1037	197.6	21.8	59287	19	US-10-741-601-5786	1110	197.2	21.7	705	13	US-10-027-632-32526	
C	1038	197.6	21.8	96649	10	US-09-956-71-12-10	1111	197.2	21.7	705	13	US-10-027-632-10432	
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C	1041	197.6	21.8	175737	22	US-10-783-71-34	1114	197.2	21.7	8397	9	US-09-828-545-37	
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C	1044	197.6	21.8	260209	15	US-10-025-966-23	1117	197.2	21.7	2818	20	US-10-602-494-25	
C	1045	197.6	21.8	326014	9	US-09-731-231A-3	1118	197.2	21.7	2969	15	US-10-177-233-301	
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C	1047	197.4	21.8	463	10	US-09-918-995-23846	1120	197.2	21.7	8397	9	US-09-828-545-37	
C	1048	197.4	21.8	469	19	US-10-674-124-9743	1121	197.2	21.7	8397	20	US-10-668-800-37	
C	1049	197.4	21.8	588	17	US-10-12-697-1413	1122	197.2	21.7	16156	15	US-10-017-161-981	
C	1050	197.4	21.8	600	21	US-10-956-157-7352	1123	197.2	21.7	22047	21	US-10-417-177-371-12	
C	1051	197.4	21.8	602	13	US-10-027-632-129993	1124	197.2	21.7	22056	19	US-10-322-281-106	
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c1132	197	21.7	96888	17	US-10-085-117-76	Sequence 76, Appli	c1205	196.6	21.7	461	10	US-09-827-271-3
c1133	197	21.7	114331	13	US-10-087-122-862	Sequence 862, App	c1206	196.6	21.7	461	15	US-10-198-053-1
c1134	197	21.7	116792	13	US-10-087-121-1090	Sequence 1090, App	c1207	196.6	21.7	461	15	US-10-198-053-3
c1135	197	21.7	119501	17	US-10-174-319-15	Sequence 15, Appli	c1208	196.6	21.7	461	21	US-10-860-790-1
c1136	197	21.7	119596	14	US-10-270-316-3	Sequence 3, Appli	c1209	196.6	21.7	461	21	US-10-860-790-3
c1137	197	21.7	128034	17	US-10-282-174-185	Sequence 185, App	c1210	196.6	21.7	571	13	US-10-027-632-252752
c1138	197	21.7	128034	17	US-10-282-174-187	Sequence 187, App	c1211	196.6	21.7	571	17	US-10-027-632-252752
c1139	197	21.7	128034	21	US-10-600-009-186	Sequence 186, App	c1212	196.6	21.7	2255	13	US-10-027-632-110965
c1140	197	21.7	128034	21	US-10-600-009-187	Sequence 187, App	c1213	196.6	21.7	2255	17	US-10-027-632-110965
c1141	197	21.7	136336	22	US-10-156-149-3773	Sequence 3773, App						Sequence 252752,
c1142	197	21.7	155974	13	US-10-026-188-6	Sequence 6, Appli						Sequence 110965,
c1143	197	21.7	165181	20	US-10-723-800-1452	Sequence 1452, App						Sequence 252752,
c1144	197	21.7	166881	20	US-10-723-800-3281	Sequence 3281, App						Sequence 110965,
c1145	197	21.7	174448	13	US-10-087-132-148	Sequence 148, App						Sequence 252752,
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c1147	197	21.7	212031	13	US-10-087-152-1126	Sequence 1126, App						Sequence 252752,
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c1152	196.8	21.7	887	13	US-10-027-632-156972	Sequence 156974, App						Sequence 110965,
c1153	196.8	21.7	887	17	US-10-027-632-156973	Sequence 156973, App						Sequence 252752,
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c1155	196.8	21.7	887	17	US-10-027-632-156974	Sequence 156974, App						Sequence 252752,
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c1162	196.8	21.7	7444	10	US-09-764-831-8806	Sequence 8806, App						Sequence 110965,
c1163	196.8	21.7	7444	10	US-09-764-831-9448	Sequence 9448, App						Sequence 252752,
c1164	196.8	21.7	7444	10	US-10-091-414-316	Sequence 316, App						Sequence 110965,
c1165	196.8	21.7	9765	9	US-09-764-855-888	Sequence 888, App						Sequence 252752,
c1166	196.8	21.7	9765	9	US-09-764-855-935	Sequence 935, App						Sequence 110965,
c1167	196.8	21.7	9765	14	US-10-091-414-248	Sequence 248, App						Sequence 252752,
c1168	196.8	21.7	9765	14	US-10-091-414-257	Sequence 257, App						Sequence 110965,
c1169	196.8	21.7	9765	14	US-10-091-414-257	Sequence 257, App						Sequence 252752,
c1170	196.8	21.7	9765	14	US-10-091-414-257	Sequence 257, App						Sequence 110965,
c1171	196.8	21.7	27047	14	US-10-292-758-621	Sequence 27047, App						Sequence 252752,
c1172	196.8	21.7	32292	9	US-09-764-857-3657	Sequence 3657, App						Sequence 110965,
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c1176	196.8	21.7	354541	17	US-10-085-117-184	Sequence 2765, App						Sequence 110965,
c1177	196.8	21.7	354541	21	US-10-843-611A-2765	Sequence 701, App						Sequence 252752,
c1178	196.8	21.7	37025	11	US-10-741-600-17653	Sequence 17653, A						Sequence 110965,
c1179	196.8	21.7	39105	21	US-10-741-600-17653	Sequence 226, App						Sequence 252752,
c1180	196.8	21.7	44225	11	US-09-997-722-226	Sequence 38, Appli						Sequence 110965,
c1181	196.8	21.7	45544	19	US-10-367-034-38	Sequence 184, App						Sequence 252752,
c1182	196.8	21.7	5963	17	US-10-085-117-184	Sequence 88, Appli						Sequence 110965,
c1183	196.8	21.7	67553	22	US-10-737-032-88	Sequence 88, Appli						Sequence 252752,
c1184	196.8	21.7	67553	22	US-10-765-730-88	Sequence 88, Appli						Sequence 110965,
c1185	196.8	21.7	67558	21	US-10-741-600-1774	Sequence 1774, A						Sequence 252752,
c1186	196.8	21.7	70000	20	US-10-476-931-3	Sequence 3, Appli						Sequence 110965,
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c1188	196.8	21.7	106338	19	US-10-322-201-566	Sequence 566, App						Sequence 110965,
c1189	196.8	21.7	116327	20	US-10-719-933-6857	Sequence 6867, App						Sequence 252752,
c1190	196.8	21.7	145906	20	US-10-719-933-6843	Sequence 6943, App						Sequence 110965,
c1191	196.8	21.7	158001	17	US-10-111-179-11	Sequence 1794, A						Sequence 252752,
c1192	196.8	21.7	165997	22	US-10-737-032-77	Sequence 77, Appli						Sequence 110965,
c1193	196.8	21.7	165997	22	US-10-765-710-77	Sequence 77, Appli						Sequence 252752,
c1194	196.8	21.7	201339	21	US-10-278-638-246	Sequence 246, App						Sequence 110965,
c1195	196.8	21.7	201339	21	US-10-278-638-760	Sequence 760, App						Sequence 252752,
c1196	196.8	21.7	414395	20	US-10-719-933-6876	Sequence 6876, App						Sequence 110965,
c1197	196.8	21.7	606398	20	US-10-719-933-6782	Sequence 6782, App						Sequence 252752,
c1198	196.8	21.7	288	14	US-10-115-278-2	Sequence 2, Appli						Sequence 110965,
c1199	196.8	21.7	288	20	US-10-762-966-2	Sequence 2, Appli						Sequence 252752,
c1200	196.8	21.7	461	9	US-09-834-441-1	Sequence 1, Appli						Sequence 110965,
c1201	196.6	21.7	461	9	US-09-834-441-3	Sequence 3, Appli						Sequence 252752,
c1202	196.6	21.7	461	10	US-09-907-939-1	Sequence 1, Appli						Sequence 110965,
c1203	196.6	21.7	461	10	US-09-907-939-3	Sequence 3, Appli						Sequence 252752,
c1204	196.6	21.7	461	10	US-09-827-271-1	Sequence 1, Appli						Sequence 110965,

Search completed: September 15, 2005, 20:27:59

Job time : 867 secs

Run on: September 15, 2005, 13:47:33 ; Search time 617 Seconds
 (without alignments) 6
 8702.116 Million cell updates/sec

Title: US-09-989-733-398
 Perfect score: 907
 Sequence: 1 gggtctggatggccaa... .gtgagactccatctcacaca 907
 Scoring table: IDENTITY_NUC
 Gapext 1.0 , Gapext 1.0

Searched: 439026 seqs, 295981667 residues
 Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 1500 summaries
 N_GeneSeq_16Dec04:
 1: geneseqn1980b: *
 2: geneseqn1990b: *
 3: geneseqn2000b: *
 4: geneseqn2001ab: *
 5: geneseqn2001bs: *
 6: geneseqn2002as: *
 7: geneseqn2002bs: *
 8: geneseqn2003ab: *
 9: geneseqn2003bs: *
 10: geneseqn2003ca: *
 11: geneseqn2003ds: *
 12: geneseqn2004as: *
 13: geneseqn2004bs: *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description
RESULT 1	100.0%	standard; cDNA; 907 BP.				
ID	AJ265100	Membrane-bound protein PRO1187 encoding cDNA.				
DE	W09963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%	Score 907; DB 3; Length 907;				
Best Local Similarity	100.0%	Pred. No. 2.6e-250;				
RESULT 2	100.0%	standard; cDNA; 907 BP.				
ID	AJ453837	Human PRO1187 nucleotide sequence SEQ ID NO:54.				
DE	WO200533755-A2.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%	Score 907; DB 3; Length 907;				
Best Local Similarity	100.0%	Pred. No. 2.6e-250;				
RESULT 3	100.0%	standard; cDNA; 907 BP.				
ID	AJR44246	Human PRO1187 (UNO601) nucleotide sequence SEQ ID NO:398.				
DE	WO20073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%	Score 907; DB 5; Length 907;				
Best Local Similarity	100.0%	Pred. No. 2.6e-250;				
RESULT 4	100.0%	standard; cDNA; 907 BP.				
ID	ABK33584	CDNA encoding human PRO protein, seq ID NO 97.				
DE	WO20020288-A2.					
PD	31-JAN-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%	Score 907; DB 6; Length 907;				
Best Local Similarity	100.0%	Pred. No. 2.6e-250;				
RESULT 5	100.0%	standard; cDNA; 907 BP.				
ID	ACM64425	Novel human secreted and transmembrane protein PRO1187 cDNA.				
DE	US20030103531-A1.					
PD	02-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%	Score 907; DB 8; Length 907;				
Best Local Similarity	100.0%	Pred. No. 2.6e-250;				
RESULT 6	100.0%	standard; cDNA; 907 BP.				
ID	ABX17167	Human pro polyneurotropin #124.				
DE	US2003017476-A1.					
PD	23-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%	Score 907; DB 8; Length 907;				
Best Local Similarity	100.0%	Pred. No. 2.6e-250;				
RESULT 13	100.0%	standard; cDNA; 907 BP.				
ID	ACM17167	Novel human secreted and transmembrane protein PRO1187 cDNA.				
DE	US200223463-A1.					
PD	05-SEP-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%	Score 907; DB 8; Length 907;				
Best Local Similarity	100.0%	Pred. No. 2.6e-250;				
RESULT 14	100.0%	standard; cDNA; 907 BP.				
ID	ACM68022	Novel human secreted and transmembrane protein PRO1187 cDNA.				
DE	US2002237716-A1.					
PD	28-NOV-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%	Score 907; DB 9; Length 907;				
Best Local Similarity	100.0%	Pred. No. 2.6e-250;				
RESULT 15	100.0%	standard; cDNA; 907 BP.				
ID	ACM8471	Human secreted and transmembrane polypeptide PRO1187 cDNA.				
DE	US2002237716-A1.					

PN US2002197615-A1.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match Best Local Similarity 100.0%; Score 907; DB 9; Length 907;
 RESULT 15 ID ACD81978 standard; cDNA; 907 BP.
 DE cDNA encoding human PRO1187 polypeptide.
 PN US2003017981-A1.
 PD 23-JAN-2003.

Query Match Best Local Similarity 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 17 ID ABT4274 standard; cDNA; 907 BP.
 DE Human PRO187 cDNA.
 PN US2003050494-A1.

PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match Best Local Similarity 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 18 ID ADA37909 standard; cDNA; 907 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1187.
 PN US2003008227-A1.
 PD 09-JAN-2003.

Query Match Best Local Similarity 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 19 ID ADA21595 standard; cDNA; 907 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO1187.
 PN US2003054494-A1.
 PD 27-MAR-2003.
 Query Match Best Local Similarity 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 20 ID ADA10382 standard; cDNA; 907 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1187.
 PN US2003059831-A1.
 PD 27-MAR-2003.

Query Match Best Local Similarity 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 21 ID ADA17926 standard; cDNA; 907 BP.
 DE cDNA encoding human PRO1187 polypeptide.
 PN US2003054987-A1.
 PD 20-MAR-2003.

Query Match Best Local Similarity 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 22 ID ADA28034 standard; cDNA; 907 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1187.
 PN US2003054339-A1.
 PD 20-MAR-2003.

Query Match Best Local Similarity 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 23 ID ADA49414 standard; cDNA; 907 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1187.
 PN US2003059832-A1.
 PD 27-MAR-2003.

Query Match Best Local Similarity 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 24 ID ADA38939 standard; cDNA; 907 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1187.
 PN US2003059790-A1.
 PD 27-MAR-2003.

Query Match Best Local Similarity 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 25 ID ABT44557 standard; cDNA; 907 BP.
 DE Human PRO1187 cDNA.
 PN US2003059790-A1.
 PD 17-APR-2003.

Query Match Best Local Similarity 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 34 ID ADB81587 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003073814-A1.
 PD 17-APR-2003.

Query Match Best Local Similarity 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 35 ID ADBB0693 standard; cDNA; 907 BP.
 DE Human PRO1187 cDNA.

DB Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003088008-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Best Local Similarity 100.0%; Score 907; DB 9; Length 907;
 RESULT 36 ID ADB73234 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003096988-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 37 ID ADB9606 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #124.
 PN US2003054433-A1.
 PD 20-MAR-2003.
 Query Match 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 38 ID ADB78316 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003092389-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 39 ID ADB8464 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #49.
 PN US2003073817-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 40 ID ADB87070 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003092886-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 41 ID ADB87136 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #49.
 PN US2003098867-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 42 ID ADB84718 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #49.
 PN US2003092890-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 43 ID ADB83833 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003093997-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 44 ID ADB72988 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003092887-A1.

PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 45 ID ADC5788 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #124.
 PN US2003027754-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 46 ID ADC55242 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #124.
 PN US2003045463-A1.
 PD 06-MAR-2003.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 47 ID ADC12109 standard; cDNA; 907 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1187.
 PN US2003049681-A1.
 PD 13-MAR-2003.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 48 ID ADC56531 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #124.
 PN US2003064375-A1.
 PD 03-APR-2003.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 49 ID ADC7186 standard; cDNA; 907 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1187.
 PN US20030647-A1.
 PD 10-APR-2003.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 50 ID ADC11576 standard; cDNA; 907 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1187.
 PN US2003069403-A1.
 PD 10-APR-2003.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 51 ID ADC36806 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #49.
 PN US2003088065-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 52 ID ADC21816 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #49.
 PN US2003096969-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 53 ID ADC49847 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003098054-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 54 ID ADC49045 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.

PN US2003088070-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 55
 ID ADC49563 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003088071-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 56
 ID ADC7424 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003088072-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 57
 ID ADC14698 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US200308246-A1.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 58
 ID ADC47169 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US200310528-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 59
 ID ADC80230 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003068623-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 60
 ID ADC80230 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003083461-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 61
 ID ADC80230 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #124.
 PN US200219339-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 62
 ID ADD07697 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US200219339-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 63
 ID ADC78044 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003096972-A1.
 PD 22-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 64
 ID ADC78044 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003096972-A1.
 PD 22-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 65
 ID ADC77798 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003073090-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 66
 ID ADC77798 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US200308066-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 67
 ID ADD07017 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2002193300-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 68
 ID ADC8264 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #124.
 PN US2003059783-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 69
 ID ADD07071 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003105291-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 70
 ID ADD51007 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003105290-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 71
 ID ADD55371 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #124.
 PN US2003077593-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 72
 ID ADD6329 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #124.
 PN US2003077594-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 10; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 73
 ID ADD0488 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #49.
 PN US2003096571-A1.
 PD 22-MAY-2003.

PA (GETH) GENENTECH INC. 100.0%; Score 907; DB 10; Length 907;
 Query Match Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 74
 ID ADD54767 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #124.
 PN US2002132253-A1.
 PD 19-SEP-2002.

PA (GETH) GENENTECH INC. 100.0%; Score 907; DB 10; Length 907;
 Query Match Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 75
 ID ADD50242 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #49.
 PN US2003096910-A1.
 PD 22-MAY-2003.

PA (GETH) GENENTECH INC. 100.0%; Score 907; DB 10; Length 907;
 Query Match Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 76
 ID ADD51253 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003105299-A1.
 PD 05-JUN-2003.

PA (GETH) GENENTECH INC. 100.0%; Score 907; DB 10; Length 907;
 Query Match Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 77
 ID ADE26221 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003045637-A1.
 PD 08-MAY-2003.

Query Match Best Local Similarity 100.0%; Score 907; DB 10; Length 907;
 RESULT 78
 ID ADP26308 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003087304-A1.
 PD 08-MAY-2003.

Query Match Best Local Similarity 100.0%; Score 907; DB 10; Length 907;
 RESULT 79
 ID ADP67125 standard; cDNA; 907 BP.
 DE Human PRO1187 nucleotide sequence SEQ ID NO:398.
 PN US2002198148-A1.
 PD 26-DEC-2002.

PA (GETH) GENENTECH INC. 100.0%; Score 907; DB 10; Length 907;
 Query Match Best Local Similarity 100.0%; Score 907; DB 10; Length 907;
 RESULT 80
 ID ADP35579 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #124.
 PN US2003050457-A1.
 PD 13-MAR-2003.

Query Match Best Local Similarity 100.0%; Score 907; DB 10; Length 907;
 RESULT 81
 ID ADP0072 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003049682-A1.
 PD 13-MAR-2003.

Query Match Best Local Similarity 100.0%; Score 907; DB 10; Length 907;
 RESULT 82
 ID ABX7968 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #124.
 PN US200307163-A1.
 PD 06-FEB-2003.

Query Match Best Local Similarity 100.0%; Score 907; DB 10; Length 907;
 RESULT 83
 ID ACM69286 standard; cDNA; 907 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1187.
 PN US2003100717-A1.
 PD 29-MAY-2003.

PN US2003032023-A1.
 PD 13-FEB-2003.
 Query Match Best Local Similarity 100.0%; Score 907; DB 10; Length 907;
 RESULT 84
 ID ARX9157 standard; cDNA; 907 BP.
 DE Human secreted/transmembrane protein cDNA, #160.
 PN US2002160384-A1.
 PD 31-OCT-2002.

PA (GETH) GENENTECH INC. 100.0%; Score 907; DB 10; Length 907;
 Query Match Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 85
 ID ACA6689 standard; cDNA; 907 BP.
 DE cDNA encoding human PRO polypeptide #49.
 PN US2003036635-A1.
 PD 20-FEB-2003.

PA (GETH) GENENTECH INC. 100.0%; Score 907; DB 10; Length 907;
 Query Match Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 86
 ID AC6841 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003045637-A1.
 PD 06-MAR-2003.

PA (GETH) GENENTECH INC. 100.0%; Score 907; DB 10; Length 907;
 Query Match Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 87
 ID ARX6403 standard; cDNA; 907 BP.
 DE cDNA encoding human PRO1187 polypeptide.
 PN US2002103125-A1.
 PD 01-AUG-2002.

PA (GETH) GENENTECH LTD. 100.0%; Score 907; DB 10; Length 907;
 Query Match Best Local Similarity 100.0%; Score 907; DB 10; Length 907;
 RESULT 88
 ID ADC4880 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003092886-A1.
 PD 15-MAY-2003.

PA (GETH) GENENTECH INC. 100.0%; Score 907; DB 10; Length 907;
 Query Match Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 89
 ID ADB20971 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003100735-A1.
 PD 29-MAY-2003.

PA (GETH) GENENTECH INC. 100.0%; Score 907; DB 12; Length 907;
 Query Match Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 90
 ID ADB05815 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #49.
 PN US2003100728-A1.
 PD 28-MAY-2003.

PA (GETH) GENENTECH INC. 100.0%; Score 907; DB 12; Length 907;
 Query Match Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 91
 ID ADD7504 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #49.
 PN US2003100711-A1.
 PD 29-MAY-2003.

PA (GETH) GENENTECH INC. 100.0%; Score 907; DB 12; Length 907;
 Query Match Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 92
 ID ADD75790 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003100717-A1.
 PD 29-MAY-2003.

Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 111
 ID ADD8602 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003100719-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 112
 ID ADD78070 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003100731-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Best Local Similarity 100.0%; Score 907; DB 12; Length 907;
 RESULT 113
 ID ADD7778 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003100739-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 114
 ID ADD7724 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003100740-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 115
 ID ADD85282 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003100755-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Best Local Similarity 100.0%; Score 907; DB 12; Length 907;
 RESULT 116
 ID ADD7814 standard; cDNA; 907 BP.
 DE Human PRO polyneucleotide #49.
 PN US2003100770-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 117
 ID ADD74552 standard; cDNA; 907 BP.
 DE Human PRO polyneucleotide #49.
 PN US2003100771-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 118
 ID ADD77080 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003100776-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 119
 ID ADD85774 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003100779-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 120
 ID AD80323 standard; cDNA; 907 BP.
 DE Human PRO Polyneucleotide #49.
 PN US2003100773-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 121
 ID ADD74798 standard; cDNA; 907 BP.
 DE Human PRO polyneucleotide #49.
 PN US2003100724-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 122
 ID ADP3524 standard; cDNA; 907 BP.
 DE cDNA encoding human PRO1187 polypeptide.
 PN US2003194760-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 123
 ID ADG11774 standard; cDNA; 907 BP.
 DE cDNA encoding human PRO1187 polypeptide.
 PN US2003228655-A1.
 PD 11-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 124
 ID ADG05610 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003096939-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 125
 ID ADG27164 standard; cDNA; 907 BP.
 DE Human PRO polyneucleotide #49.
 PN US2003096965-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 126
 ID ADG1127 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003096967-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 127
 ID ADG12006 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003096963-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 128
 ID ADP94553 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003096964-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 129
 ID ADG06659 standard; cDNA; 907 BP.

DE Human PRO Polynucleotide #49.
 PN US2003036966-A1.
 PD 22-MAY-2003.
 PA (GETH-) GENENTECH INC.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 130
 ID AD13903 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2003036965-A1.
 PD 22-MAY-2003.
 PA (GETH-) GENENTECH INC. 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 131
 ID ADH19644 standard; cDNA; 907 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1187.
 PN US2003228656-A1.
 PD 11-DEC-2003.
 PA (GETH-) GENENTECH INC. 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 132
 ID ADH21137 standard; cDNA; 907 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1187.
 PN US2003224358-A1.
 PD 04-DEC-2003.
 Query Match 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 133
 ID ADH20177 standard; cDNA; 907 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1187.
 PN US2003219856-A1.
 PD 27-NOV-2003.
 PA (GETH-) GENENTECH INC. 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 134
 ID ADG34093 standard; cDNA; 907 BP.
 DE Novel human Secreted and transmembrane protein PRO1187 cDNA.
 PN US2004006206-A1.
 PD 08-JAN-2004.
 PA (GETH-) GENENTECH INC. 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 135
 ID AD13563 standard; cDNA; 907 BP.
 DE Human PRO Polynucleotide #49.
 PN US2003036960-A1.
 PD 22-MAY-2003.
 PA (GETH-) GENENTECH INC. 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 136
 ID AD16957 standard; cDNA; 907 BP.
 DE Human PRO Polynucleotide #49.
 PN US2004019183-A1.
 PD 29-JAN-2004.
 PA (GETH-) GENENTECH INC. 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 137
 ID AD129818 standard; cDNA; 907 BP.
 DE Novel human Secreted and transmembrane protein PRO1187 cDNA.
 PN US2003036961-A1.
 PD 22-MAY-2003.
 PA (GETH-) GENENTECH INC. 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 138
 ID ADM27215 standard; cDNA; 907 BP.
 DE Novel human secreted and transmembrane protein PRO1187 cDNA.
 PN US2004044179-A1.
 PD 04-MAR-2004.
 PA (GETH-) GENENTECH INC. 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 139
 ID ADK6573 standard; cDNA; 907 BP.
 DE Human PRO polynucleotide #49.
 PN US2004041180-A1.
 PD 04-MAR-2004.
 PA (GETH-) GENENTECH INC. 100.0%; Score 907; DB 12; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 RESULT 140
 ID ABK02709 standard; DNA; 17761 BP.
 DE Genomic sequence #608 encoding novel human connective tissue polypeptide.
 PN WO2001155343-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. 100.0%; Score 907; DB 4; Length 17761;
 Best Local Similarity 100.0%; Pred. No. 8.3e-250;
 RESULT 141
 ID AAK19415 standard; DNA; 17761 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34227.
 PN WO200151782-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. 100.0%; Score 907; DB 4; Length 17761;
 Best Local Similarity 100.0%; Pred. No. 8.3e-250;
 RESULT 142
 ID ADB0865 standard; DNA; 17761 BP.
 DE Connective tissue related genomic DNA #608.
 PN US2003054375-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC. 100.0%; Score 907; DB 9; Length 17761;
 Best Local Similarity 100.0%; Pred. No. 8.3e-250;
 RESULT 143
 ID ABZ1132 standard; cDNA; 1154 BP.
 DE Human Polynucleotide SEQ ID NO 204.
 PN WO2002705339-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC. 66.3%; Score 601.6; DB 6; Length 1154;
 Best Local Similarity 99.3%; Pred. No. 2e-162;
 RESULT 144
 ID ADM3840 standard; cDNA; 1154 BP.
 DE Novel human arginine-rich protein cDNA #204.
 PN US2004053250-A1.
 PD 18-MAR-2004.
 PA (TANG-) TANG Y T.
 PA (XRAY-) XTE A.
 PA (DRNA-) DRMANAC R T. 66.3%; Score 601.6; DB 12; length 1154;
 Query Match 66.3%; Score 601.6; DB 12; length 1154;
 Best Local Similarity 99.3%; Pred. No. 2e-162;
 RESULT 145
 ID AAF0563 standard; cDNA; 500 BP.
 DE Receptor #51 partial coding sequence.
 PN US6183968-B1.
 PD 06-FEB-2001.
 PA (INCY-) INCYTE PHARM INC. 55.1%; Score 500; DB 4; Length 500;
 Best Local Similarity 100.0%; Pred. No. 2.4e-133;
 RESULT 146
 ID ABL02546 standard; cDNA; 480 BP.
 DE Human ovarian cancer related cDNA clone SEQ ID NO:5524.
 PN WO200192581-A2.
 PD 06-DEC-2001.
 PA (CORT-) CORIXA CORP. 50.5%; Score 458; DB 6; Length 480;
 Query Match 50.5%; Score 458; DB 6; Length 480;
 Best Local Similarity 99.6%; Pred. No. 2.9e-121;
 RESULT 147
 ID ABU189 standard; cDNA; 425 BP.
 DE Human ovarian cancer related cDNA clone SEQ ID NO:3167.

DN Human cardiovascular system associated polypeptide-related DNA SeqID1390.
 PN US20040105575-A1.
 PD 08-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity 23.5%; Score 213; DB 13; Length 10093;
 RESULT 157
 ID AAL04218 standard; DNA; 32148 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 6906.
 PN WO20015320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.5%; Score 212.8; DB 4; Length 32148;
 Best Local Similarity 83.8%; Pred. No. 4.8e-50;
 RESULT 158
 ID AAS36445 standard; DNA; 17397 BP.
 DE Human cardiovascular system antigen genomic DNA SEQ ID No 1945.
 PN WO20155321-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.4%; Score 212.2; DB 4; Length 17397;
 Best Local Similarity 73.6%; Pred. No. 5.7e-50;
 RESULT 159
 ID ABE47139 standard; DNA; 17397 BP.
 DE Human cardiovascular system related genomic DNA #705.
 PN US2003059908-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.4%; Score 212.2; DB 10; Length 17397;
 Best Local Similarity 73.6%; Pred. No. 5.7e-50;
 RESULT 160
 ID ABE08557 standard; DNA; 17397 BP.
 DE Human cardiovascular system associated polypeptide-related DNA SeqID1945.
 PN US20040105575-A1.
 PD 08-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.4%; Score 212.2; DB 13; Length 17397;
 Best Local Similarity 73.6%; Pred. No. 5.7e-50;
 RESULT 161
 ID AAS36443 standard; DNA; 19334 BP.
 DE Human cardiovascular system antigen genomic DNA SEQ ID No 1943.
 PN WO20015321-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.4%; Score 212.2; DB 4; Length 19334;
 Best Local Similarity 73.6%; Pred. No. 5.9e-50;
 RESULT 162
 ID ABE47137 standard; DNA; 19334 BP.
 DE Human cardiovascular system related genomic DNA #703.
 PN US2003059908-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.4%; Score 212.2; DB 10; Length 19334;
 Best Local Similarity 73.6%; Pred. No. 5.9e-50;
 RESULT 163
 ID ABO8555 standard; DNA; 19334 BP.
 DE Human cardiovascular system associated polypeptide-related DNA SeqID1943.
 PN US20040105575-A1.
 PD 08-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.4%; Score 212.2; DB 13; Length 19334;
 Best Local Similarity 73.6%; Pred. No. 5.9e-50;
 RESULT 164
 ID AAS3644 standard; DNA; 19345 BP.
 DE Human cardiovascular system antigen genomic DNA SEQ ID No 1944.
 PN WO20015321-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.4%; Score 212.2; DB 4; Length 19345;
 Best Local Similarity 73.6%; Pred. No. 5.9e-50;
 RESULT 165
 ID ADE47138 standard; DNA; 19345 BP.
 DE Human cardiovascular system related genomic DNA #704.

PN WO200192581-A2.
 PD 06-DEC-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 44.4%; Score 403; DB 6; Length 425;
 Best Local Similarity 99.5%; Pred. No. 1.8e-105;
 RESULT 148
 ID ABL0621 standard; cDNA; 402 BP.
 DE Human ovarian cancer related cDNA clone SEQ ID NO:3599.
 PN WO200192581-A2.
 PD 06-DEC-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 40.7%; Score 369; DB 6; Length 402;
 Best Local Similarity 99.3%; Pred. No. 1.1e-95;
 RESULT 149
 ID ABL83135 standard; cDNA; 360 BP.
 DE Human ovarian cancer related cDNA clone SEQ ID NO:6113.
 PN WO200192581-A2.
 PD 06-DEC-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 37.9%; Score 344.2; DB 6; Length 360;
 Best Local Similarity 98.9%; Pred. No. 1.4e-88;
 RESULT 150
 ID AUF66312 standard; cDNA; 399 BP.
 DE Novel human polynucleotide, SEQ ID NO: 2068.
 PN WO200102568-A2.
 PD 11-JAN-2001.
 PA (CHIR-) CHIRION CORP.
 Query Match 24.6%; Score 222.8; DB 5; Length 399;
 Best Local Similarity 99.1%; Pred. No. 1.2e-53;
 RESULT 151
 ID AUF66311 standard; cDNA; 395 BP.
 DE Novel human polynucleotide, SEQ ID NO: 2067.
 PN WO200102568-A2.
 PD 11-JAN-2001.
 PA (CHIR-) CHIRION CORP.
 Query Match 23.8%; Score 215.6; DB 5; Length 395;
 Best Local Similarity 98.2%; Pred. No. 1.4e-51;
 RESULT 152
 ID AAS35890 standard; DNA; 10093 BP.
 DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1390.
 PN WO2001025206-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.5%; Score 213; DB 4; Length 10093;
 Best Local Similarity 85.8%; Pred. No. 2.7e-50;
 RESULT 153
 ID ABA07184 standard; DNA; 10093 BP.
 DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 503.
 PN WO2001025206-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.5%; Score 213; DB 4; Length 10093;
 Best Local Similarity 85.8%; Pred. No. 2.7e-50;
 RESULT 154
 ID AAK9816 standard; DNA; 10093 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3392.
 PN WO2001025314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.5%; Score 213; DB 4; Length 10093;
 Best Local Similarity 85.8%; Pred. No. 2.7e-50;
 RESULT 155
 ID AAK9816 standard; DNA; 10093 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3392.
 PN WO2001025314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.5%; Score 213; DB 4; Length 10093;
 Best Local Similarity 85.8%; Pred. No. 2.7e-50;
 RESULT 156
 ID ADR46584 standard; DNA; 10093 BP.
 DE Human cardiovascular system related genomic DNA #150.
 PN US2003059908-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.5%; Score 213; DB 4; Length 10093;
 Best Local Similarity 85.8%; Pred. No. 2.7e-50;
 RESULT 157
 ID ADJ08002 standard; DNA; 10093 BP.
 DE Human cardiovascular system related genomic DNA #704.

PN US2003059908-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC. 23.4%; Score 212.2; DB 10; Length 19345;
 Query Match Best Local Similarity 73.6%; Pred. No. 5.9e-50;
 RESULT 166 ADJ08556 standard; DNA; 19345 BP.
 DE Human cardiovascular system associated polypeptide-related DNA SeqID1944.
 ID (AMHP) WHEW.
 DE (TWIN/) TWINE N.C.
 PA (BURN/) BURCZYNSKI M.E.
 PA (TREP/) TREPICCHIO W.L.
 PA (DORN/) DORNER A.
 PA (STOV/) STOVER J.A.
 PN US20040555-A1.
 PD 08-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC. 23.4%; Score 212.2; DB 13; Length 19345;
 Query Match Best Local Similarity 73.6%; Pred. No. 5.9e-50;
 RESULT 167 ADP0557 standard; DNA; 29001 BP.
 DE Human zinein polynucleotide.
 ID ACN44806 standard; DNA; 177587 BP.
 DE Human genomic sequence hCG40093.
 PN WO2003073866-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGES DISCOVERY. Query Match Best Local Similarity 23.4%; Score 211.8; DB 11; Length 29001;
 RESULT 168 Best Local Similarity 73.6%; Pred. No. 6.9e-50;
 DE Human genomic sequence hCG30014.
 PN WO2003073866-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SACRES DISCOVERY. Query Match Best Local Similarity 23.4%; Score 211.6; DB 11; Length 118931;
 Best Local Similarity 86.0%; Pred. No. 1.8e-49;
 RESULT 169 DE ACN44806 standard; DNA; 118931 BP.
 DE Human genomic sequence hCG30014.
 PN WO2003073866-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. Query Match Best Local Similarity 23.2%; Score 210; DB 12; Length 126990;
 DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:34716.
 PN WO2003027328-A2.
 PD 03-APR-2003.
 PA (BOST-) BOSTON PROBES INC. Query Match Best Local Similarity 80.2%; Pred. No. 3.5e-49;
 DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:34716.
 PN WO200307182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. Query Match Best Local Similarity 23.2%; Score 210; DB 10; Length 301;
 DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:60.
 PN WO20030116311-A1.
 PD 08-MAR-2001.
 PA (HISM-) HISAMITSU PHARM CO LTD. Query Match Best Local Similarity 82.6%; Pred. No. 1.4e-49;
 DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:60.
 PN WO2003022899-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC. Query Match Best Local Similarity 82.8%; Pred. No. 4.2e-49;
 DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:60.
 PN WO200305367-A1.
 PA (HUMA-) HUMAN GENOME SCI INC. Query Match Best Local Similarity 85.1%; Pred. No. 5.9e-49;
 DE Human nervous system related polynucleotide SEQ ID NO 3220.
 PN WO2003042056-A1.
 PD 11-APR-2002.
 PA (ROSE-) ROSEN C A. Query Match Best Local Similarity 86.7%; Pred. No. 3.8e-49;
 DE Human liver-associated genomic DNA #311.
 PN WO200305367-A1.
 PD 02-AUG-2001.
 PA (RUBB-) RUBASH S C. Query Match Best Local Similarity 23.1%; Score 209.4; DB 4; Length 19616;
 DE Human liver antigen HFVIC84 genomic sequence, SEQ ID NO:613.
 PN WO2003077602-A1.
 ID ABN90492 standard; DNA; 24664 BP.
 DE Human liver antigen HFVIC84 genomic sequence, SEQ ID NO:613.
 RESULT 172 Best Local Similarity 83.8%; Pred. No. 1.3e-49;
 DE Human liver antigen HFVIC84 genomic sequence, SEQ ID NO:613.
 ID ADJ15405 standard; DNA; 24664 BP.
 DE Human liver-related genomic DNA - SEQ ID 613.
 PN US2003077602-A1.
 PD 24-APR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC. Query Match Best Local Similarity 23.3%; Score 211.2; DB 6; Length 24664;
 DE Human liver antigen HFVIC84 genomic sequence, SEQ ID NO:613.
 RESULT 173 Best Local Similarity 83.8%; Pred. No. 1.3e-49;
 DE Human liver antigen HFVIC84 genomic sequence, SEQ ID NO:613.
 ID ADJ15405 standard; DNA; 24664 BP.
 DE Human liver-related genomic DNA - SEQ ID 613.
 PN US2003077602-A1.
 PD 24-APR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC. Query Match Best Local Similarity 23.1%; Score 209.4; DB 5; Length 19616;
 DE Human nervous system related polynucleotide SEQ ID NO 9187.
 ID ABA1695 standard; DNA; 19616 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 8425.
 PN WO200305903-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. Query Match Best Local Similarity 86.7%; Pred. No. 3.8e-49;
 DE Human nervous system related polynucleotide SEQ ID NO 8425.
 ID ABA1694 standard; DNA; 19616 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 8425.
 PN WO200305903-A2.
 PD 16-AUG-2001.

PN US2002147110-A1.
 PD 10-OCT-2002.
 PA (ROSE-) ROSEN C A.
 PA (RUBE-) RUBEN S M.
 PA (BARA-) BARASH S C.
 Query Match 23.1%; Score 209.4; DB 8; Length 19616;
 Best Local Similarity 86.7%; Pred. No. 3.8e-49;
 RESULT 183
 ID ADJ30593 standard; DNA; 19616 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3220.
 PN US2004009488-A1.
 PD 15-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.4; DB 12; Length 19616;
 Best Local Similarity 86.7%; Pred. No. 3.8e-49;
 RESULT 184
 ID AAI62651 standard; DNA; 614 BP.
 DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 301.
 PN WO200155324-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity 83.3%; Pred. No. 1.1e-49;
 RESULT 185
 ID AAI6745 standard; DNA; 614 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9433.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 614;
 Best Local Similarity 83.3%; Pred. No. 1.1e-49;
 RESULT 186
 ID AAI62649 standard; DNA; 691 BP.
 DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 299.
 PN WO200155324-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 691;
 Best Local Similarity 83.3%; Pred. No. 1.2e-49;
 RESULT 187
 ID AAI6743 standard; DNA; 691 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9431.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity 83.3%; Pred. No. 1.2e-49;
 RESULT 188
 ID AAI62650 standard; DNA; 16225 BP.
 DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 300.
 PN WO200155324-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 691;
 Best Local Similarity 83.3%; Pred. No. 4e-49;
 RESULT 189
 ID AAI81913 standard; DNA; 16225 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 36725.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 16225;
 Best Local Similarity 83.3%; Pred. No. 4e-49;
 RESULT 190
 ID AAI6744 standard; DNA; 16225 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9432.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 16225;
 Best Local Similarity 83.3%; Pred. No. 4e-49;
 RESULT 191
 ID AAI830106 standard; DNA; 16225 BP.

DE Human lung antigen genomic DNA #176.
 PN WO20015303-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 5; Length 16225;
 Best Local Similarity 83.3%; Pred. No. 4e-49;
 RESULT 192
 ID ADB33443 standard; DNA; 16225 BP.
 DE Human novel lung related polypeptide DNA SEQ ID NO 370.
 PN US2003054368-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 10; Length 16225;
 Best Local Similarity 83.3%; Pred. No. 4e-49;
 RESULT 193
 ID ADA43380 standard; cDNA; 50000 BP.
 DE Human asthma associated gene, ANGB, genomic fragment #1.
 PN US2003104521-A1.
 PD 05-JUN-2003.
 PA (WHIT-) WHITTAKER P A.
 Query Match 23.1%; score 209.2; DB 6; Length 50000;
 Best Local Similarity 82.5%; Pred. No. 6.2e-49;
 RESULT 194
 ID ARB98944 standard; DNA; 50000 BP.
 DE Human asthma-associated gene ANGB, genomic DNA #1.
 PN WO200206312-A2.
 PD 24-JAN-2002.
 PA (NOVS-) NOVARTIS AG.
 Query Match 23.1%; score 209.2; DB 6; Length 50000;
 Best Local Similarity 82.5%; Pred. No. 6.2e-49;
 RESULT 195
 ID ARB42416 standard; DNA; 50065 BP.
 DE Human serine/threonine kinase DNA.
 PN US63340583-B1.
 PD 22-JAN-2002.
 PA (PEKE-) PE CORP NY.
 Query Match 23.1%; Score 209.2; DB 6; Length 59065;
 Best Local Similarity 79.7%; Pred. No. 6.6e-49;
 RESULT 196
 ID ARB41839 standard; DNA; 59065 BP.
 DE Human LIM domain kinase (LIMK) gene.
 PN US640353-B1.
 PD 11-JUN-2002.
 PA (PEKE-) PE CORP NY.
 Query Match 23.1%; Score 209.2; DB 6; Length 59065;
 Best Local Similarity 79.7%; Pred. No. 6.6e-49;
 RESULT 197
 ID ARB98727 standard; DNA; 59065 BP.
 DE Human kinase genomic DNA.
 PN US2003166215-A1.
 PD 04-SEP-2003.
 PA (PEKE-) PE CORP NY.
 Query Match 23.1%; Score 209.2; DB 10; Length 59065;
 Best Local Similarity 79.7%; Pred. No. 6.6e-49;
 RESULT 198
 ID ARB48909 standard; DNA; 59065 BP.
 DE Human kinase genomic DNA.
 PN US2004175751-A1.
 PD 09-SEP-2004.
 PA (APPL-) APPERA CORP.
 Query Match 23.1%; Score 209.2; DB 13; Length 59065;
 Best Local Similarity 79.7%; Pred. No. 6.6e-49;
 RESULT 199
 ID ARB83459 standard; cDNA; 128978 BP.
 DE Human cDNA differentially expressed in granulocytic cells #30.
 PN WO00220999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 23.1%; Score 209.2; DB 6; Length 128978;
 Best Local Similarity 79.7%; Pred. No. 9e-49;
 RESULT 200
 ID ADD54587 standard; DNA; 128978 BP.

DE Human LIM kinase (LIMK) DNA #6.
 PN WO200299048-A2.
 PD 12-DEC-2002.

Query Match Similarity 23.1%; Score 209.2; DB 8; Length 128978;
 Best Local Similarity 79.7%; Pred. No. 9e-49;
 RESULT 201.
 ID ADR52994 standard; DNA; 128978 BP.
 DE Drug therapy altered expressed gene #345.
 PN WO2004072265-A2.

PD 26-AUG-2004.
 PA (TREP-) TRIPICCHIO W L.
 PA (AMHP-) WIETH.
 PA (BURC-) BURCZYNSKI M.
 PA (TWIN-) TWINNE N.
 PA (DORN-) DORNER A J.
 PA (TREP-) TRIPICCHIO W L.
 Query Match Best Local Similarity 23.1%; Score 209.2; DB 13; Length 128978;
 Best Local Similarity 79.7%; Pred. No. 9e-49;
 RESULT 202.
 Query Match Best Local Similarity 23.0%; Score 209; DB 11; Length 110000;
 Best Local Similarity 84.4%; Pred. No. 9.6e-49;
 RESULT 203.
 ID ADQ18757 standard; DNA; 43712 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1576.
 PN WO2004048998-A2.

PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match Best Local Similarity 23.0%; Score 208.8; DB 12; Length 43712;
 Best Local Similarity 82.7%; Pred. No. 7.7e-49;
 RESULT 204.
 ID ADQ97127 standard; DNA; 73063 BP.
 DE Human cancer associated sequence HD10-034, SEQ ID 704.
 PN WO2004063034-A2.

PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match Best Local Similarity 23.0%; Score 208.8; DB 12; Length 73063;
 Best Local Similarity 85.1%; Pred. No. 9.4e-49;
 RESULT 205.
 ID ABK4912 standard; DNA; 518 BP.
 DE Genomic sequence #811 encoding novel human connective tissue polypeptide.
 PN WO200515343-A1.

PD 02-AUG-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 23.0%; Score 208.6; DB 4; Length 518;
 Best Local Similarity 83.6%; Pred. No. 1.6e-49;
 RESULT 206.
 ID AUB61068 standard; DNA; 518 BP.
 DE Connective tissue related genomic DNA #811.
 PN US2003054375-A1.

PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 23.0%; Score 208.6; DB 9; Length 518;
 Best Local Similarity 83.6%; Pred. No. 1.6e-49;
 RESULT 207.
 ID ADE82948 standard; DNA; 167163 BP.
 DE Human PVTI genomic DNA sequence.
 PN WO2003080808-A2.

PD 02-OCT-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match Best Local Similarity 23.0%; Score 208.6; DB 10; Length 167163;
 Best Local Similarity 84.6%; Pred. No. 1.5e-48;
 RESULT 208.
 ID AAK79905 standard; DNA; 2744 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34717.
 PN WO2003157182-A2.

PD 09-AUG-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 23.0%; Score 208.6; DB 10; Length 167163;
 Best Local Similarity 84.6%; Pred. No. 1.5e-48;
 RESULT 209.
 ID ADN06353 standard; DNA; 398800 BP.
 DE Human FLAP genomic DNA SEQ ID NO:1.
 PN WO2004035741-A2.

PD 29-APR-2004.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match Best Local Similarity 23.0%; Score 208.2; DB 12; Length 110000;
 Best Local Similarity 82.3%; Pred. No. 1.6e-48;
 RESULT 210.
 ID ADS9372 standard; DNA; 39800 BP.
 DE Human 5'-1-poxigenase activating protein (FLAP) gene.
 PN WO2004035746-A2.

PD 29-APR-2004.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match Best Local Similarity 23.0%; Score 208.2; DB 13; Length 110000;
 Best Local Similarity 82.3%; Pred. No. 1.6e-48;
 RESULT 211.
 ID ABL6793 standard; DNA; 291 BP.
 DE Prostate cancer related gene sequence SEQ ID NO:8130.
 PN WO2005194628-A2.

PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match Best Local Similarity 22.9%; Score 208; DB 6; Length 291;
 Best Local Similarity 87.2%; Pred. No. 1.9e-49;
 RESULT 212.
 ID ABL67475 standard; DNA; 291 BP.
 DE Thyroid cancer related gene sequence SEQ ID NO:5812.
 PN WO200194629-A2.

PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match Best Local Similarity 22.9%; Score 208; DB 6; Length 291;
 Best Local Similarity 87.2%; Pred. No. 1.9e-49;
 RESULT 213.
 ID ADP67956 standard; DNA; 270150 BP.
 DE Human 16p133 sequence section 7 of 8 DNA.
 PN WO2003072827-A1.

PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match Best Local Similarity 22.9%; Score 208; DB 11; Length 270150;
 Best Local Similarity 79.2%; Pred. No. 2.6e-48;
 RESULT 214.
 ID AAK71190 standard; DNA; 3139 BP.
 DE Human immune/haemopoietic antigen genomic sequence SEQ ID NO:26002.
 PN WO20051782-A2.

PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 22.9%; Score 207.8; DB 4; Length 3139;
 Best Local Similarity 78.7%; Pred. No. 5.4e-49;
 RESULT 215.
 ID ADQ20461 standard; DNA; 166181 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3281.
 PN WO2004048338-A2.

PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match Best Local Similarity 22.9%; Score 207.8; DB 12; Length 166181;
 Best Local Similarity 85.0%; Pred. No. 2.5e-48;
 RESULT 216.
 ID ADQ18633 standard; DNA; 166181 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1452.
 PN WO2004048338-A2.

PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match Best Local Similarity 22.9%; Score 207.8; DB 12; Length 166181;
 Best Local Similarity 85.0%; Pred. No. 2.5e-48;
 RESULT 217.
 ID AAD22781 standard; DNA; 31766 BP.
 DE Human sulphate transporter protein splice form genomic DNA.
 PN WO2004048338-A2.

PD 01-NOV-2001.
 PA (PEKB-) PE CORP NY.
 Query Match Best Local Similarity 22.9%; Score 207.6; DB 6; Length 31766;
 Best Local Similarity 85.8%; Pred. No. 1.5e-48;
 RESULT 218.
 ID AAL50687 standard; DNA; 31766 BP.
 DE Human sulphate transporter protein genomic DNA sequence.
 PN WO200259306-A2.

PD 01-AUG-2002.

PA (APPL-) APPLERA CORP. 22.9%; Score 207.6; DB 6; Length 31766;
 Best Local Similarity 85.8%; Pred. No. 1.5e-48;
 RESULT 219
 ID ARB8442 standard; cDNA; 43599 BP.
 DR Human cDNA differentially expressed in granulocytic cells #813.
 PN WO200228999-A2.
 PD 11-APR-2002.

PA (GENE-) GENE LOGIC INC. 22.9%; Score 207.4; DB 6; Length 43599;
 Best Local Similarity 84.0%; Pred. No. 1.9e-48;
 RESULT 220
 ID ADBI169 standard; DNA; 394191 BP.
 DR Human transporter protein encoding gene SEQ ID NO:1.
 Query Match 22.8%; Score 207.2; DB 10; Length 110000;
 Best Local Similarity 86.3%; Pred. No. 3.2e-48;
 RESULT 221
 ID ABA16169 standard; DNA; 4969 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 8500.
 PN WO200159063-A2.
 PD 16-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. 22.8%; Score 207; DB 5; Length 4969;
 Best Local Similarity 84.2%; Pred. No. 1.1e-48;
 RESULT 222
 ID ADK83502 standard; cDNA; 77425 BP.
 DE Human cDNA differentially expressed in granulocytic cells #73.
 PN WO200228999-A2.
 PD 11-APR-2002.

PA (GENE-) GENE LOGIC INC. 22.8%; Score 206.8; DB 6; Length 77425;
 Best Local Similarity 86.3%; Pred. No. 3.6e-48;
 RESULT 223
 ID ADP59434 standard; DNA; 169659 BP.
 DE Human cancer-associated (CA) gene sequence SEQ ID NO:70.
 PN WO2001058288-A1.
 PD 15-JUL-2004.

PA (SAGR-) SAGRES DISCOVERY INC. 22.8%; Score 206.8; DB 12; Length 169659;
 Best Local Similarity 79.4%; Pred. No. 4.9e-48;
 RESULT 224
 ID ADQ9721 standard; DNA; 178024 BP.
 DE Human cancer associated sequence HD10-033, SEQ ID 698.
 PN WO2004060304-A2.
 PD 22-JUL-2004.

PA (SAGR-) SAGRES DISCOVERY INC. 22.8%; Score 206.6; DB 12; Length 178024;
 Best Local Similarity 82.0%; Pred. No. 5.7e-48;
 RESULT 225
 ID ADx02756 standard; DNA; 96594 BP.
 DE Human MORP carcinoma associated gene, SEQ ID NO:1274.
 PN WO2003057146-A2.
 PD 17-JUL-2003.

PA (SAGR-) SAGRES DISCOVERY 22.8%; Score 206.4; DB 9; Length 96594;
 Best Local Similarity 84.0%; Pred. No. 5.1e-48;
 RESULT 226
 ID ADP72494 standard; DNA; 96594 BP.
 DE Human MORP gene.
 PN WO200300853-A2.
 PD 30-JAN-2003.

PA (SAGR-) SAGRES DISCOVERY 22.8%; Score 206.4; DB 10; Length 96594;
 Best Local Similarity 84.0%; Pred. No. 5.1e-48;
 RESULT 227
 ID ADG85236 standard; DNA; 96594 BP.
 DE Human Morp genomic sequence.
 PN WO2003045230-A2.
 PD 05-JUN-2003.

PA (SAGR-) SAGRES DISCOVERY 22.8%; Score 206.4; DB 10; Length 96594;
 Best Local Similarity 84.0%; Pred. No. 5.1e-48;
 RESULT 228

PA (HUMA-) HUMAN GENOME SCI INC. 22.8%; Score 206.4; DB 12; Length 96594;
 Best Local Similarity 84.0%; Pred. No. 5.1e-48;
 RESULT 229
 ID AAK84529 standard; DNA; 16146 BP.
 DR Human immune/hematopoietic antigen genomic sequence SEQ ID NO:39341.
 PN WO200157182-A2.
 PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. 22.7%; Score 206.2; DB 4; Length 16146;
 Best Local Similarity 82.2%; Pred. No. 2.9e-48;
 RESULT 230
 ID AAK8945 standard; DNA; 16146 BP.
 DR Human secreted protein-related DNA sequence #538.
 PN WO200104623-A2.
 PD 16-JAN-2003.

PA (HUMA-) HUMAN GENOME SCI INC. 22.7%; Score 206.2; DB 8; Length 16146;
 Best Local Similarity 82.2%; Pred. No. 2.9e-48;
 RESULT 231
 ID ADP44511 standard; DNA; 16146 BP.
 DR Human secreted protein DNA SEQ ID 744.
 PN WO2003000865-A2.
 PD 03-JAN-2003.

PA (HUMA-) HUMAN GENOME SCI INC. 22.7%; Score 206.2; DB 8; Length 16146;
 Best Local Similarity 82.2%; Pred. No. 2.9e-48;
 RESULT 232
 ID ADP20930 standard; DNA; 16146 BP.
 DR Human secreted protein-related DNA sequence #398.
 PN WO200222787-A2.
 PD 21-NOV-2002.

PA (HUMA-) HUMAN GENOME SCI INC. 22.7%; Score 206.2; DB 10; Length 16146;
 Best Local Similarity 82.2%; Pred. No. 2.9e-48;
 RESULT 233
 ID ADP1104 standard; DNA; 16146 BP.
 DR Human Secreted protein encoding sequence #326.
 PN WO200229085-A2.
 PD 12-DEC-2002.

PA (HUMA-) HUMAN GENOME SCI INC. 22.7%; Score 206.2; DB 10; Length 16146;
 Best Local Similarity 82.2%; Pred. No. 2.9e-48;
 RESULT 234
 ID ABT17011 standard; DNA; 16146 BP.
 DR Human secreted protein-related DNA sequence - SEQ ID NO 365.
 PN WO200277188-A2.
 PD 03-OCT-2002.

PA (HUMA-) HUMAN GENOME SCI INC. 22.7%; Score 206.2; DB 10; Length 16146;
 Best Local Similarity 82.2%; Pred. No. 2.9e-48;
 RESULT 235
 ID ABT18089 standard; DNA; 16146 BP.
 DR Human secreted protein encoding genomic DNA SEQ ID NO 1612.
 PN WO200277185-A2.
 PD 03-OCT-2002.

PA (HUMA-) HUMAN GENOME SCI INC. 22.7%; Score 206.2; DB 10; Length 16146;
 Best Local Similarity 82.2%; Pred. No. 2.9e-48;
 RESULT 236
 ID ACN4482 standard; DNA; 34996 BP.
 DR Human genomic sequence hCG66017.
 PN WO2003073826-A2.
 PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY 22.7%; Score 206.2; DB 11; Length 34096;
 Best Local Similarity 78.4%; Pred. No. 3.9e-48;
 RESULT 237

ID AAF58067 standard; DNA; 39198 BP.
 DR Human polynucleotide-modulated factor-1 gene.
 PN WO200107610-A1.

RESULT 238
 ID AAN8533 standard; DNA; 48436 BP.
 DR Human corneal N-acetylglucosamine-6-sulfotransferase DNA SEQ ID NO:38.
 PN US2002061562-A1.

PD 23-MAY-2002.
 PA (YUKO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 Best Local Similarity 84.7%; Score 206.2; DB 5; Length 39198;
 Pred. No. 4.1e-48;

RESULT 239
 ID ADL1501 standard; DNA; 157932 BP.
 DR Osteoarthritis-associated polymorphic nucleotide #33.
 PN WO2003054166-A2.

PD 03-JUL-2003.
 PA (INCY-) INCYT GENOMICS INC.
 Query Match 22.7%; Score 206.2; DB 10; Length 157932;
 Best Local Similarity 84.7%; Pred. No. 7.2e-48;
 Pred. No. 4.5e-48;

RESULT 240
 ID ABN87883 standard; DNA; 50849 BP.
 DR Human glutathione reductase (GSR) gene SEQ ID NO:1.
 PN WO200242320-A2.

PD 30-MAY-2002.
 PA (GENA-) GENNAISANCE PHARM INC.
 Query Match 22.7%; Score 206; DB 6; Length 50849;
 Best Local Similarity 81.7%; Pred. No. 5.2e-48;

RESULT 241
 ID ADQ97152 standard; DNA; 58651 BP.
 DR Human cancer associated sequence HD08-008, SEQ ID 128.
 PN WO200405034-A2.

PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.7%; Score 206; DB 12; Length 58651;
 Best Local Similarity 79.0%; Pred. No. 5.5e-48;

RESULT 242
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.7%; Score 206; DB 12; Length 87411;
 Best Local Similarity 84.4%; Pred. No. 6.4e-48;

RESULT 243
 ID ABA16120 standard; DNA; 447 BP.
 DR Human nervous system related polynucleotide SEQ ID NO 8451.
 PN WO200159053-A2.

PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.7%; Score 205.8; DB 5; Length 447;
 Best Local Similarity 84.9%; Pred. No. 9.6e-49;

RESULT 244
 ID ABA20765 standard; DNA; 447 BP.
 DR Human nervous system related polynucleotide SEQ ID NO 13096.
 PN WO200159053-A2.

PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.7%; Score 205.8; DB 5; Length 447;
 Best Local Similarity 84.9%; Pred. No. 9.6e-49;

RESULT 245
 ID AAK81748 standard; DNA; 451 BP.
 DR Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22737.
 PN WO200157182-A2.

PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.7%; Score 205.8; DB 4; Length 451;
 Best Local Similarity 84.9%; Pred. No. 9.7e-49;

RESULT 246
 ID AAK81748 standard; DNA; 451 BP.
 DR Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36560.
 PN WO200157182-A2.

PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 22.7%; Score 205.8; DB 4; Length 451;
 Best Local Similarity 84.9%; Pred. No. 9.7e-49;

RESULT 247
 ID ABA16121 standard; DNA; 451 BP.
 DR Human nervous system related polynucleotide SEQ ID NO 8452.
 PN WO200159053-A2.

PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.7%; Score 205.8; DB 5; Length 451;
 Best Local Similarity 84.9%; Pred. No. 9.7e-49;

RESULT 248
 ID AQ92779 standard; DNA; 6905 BP.
 DR Human thymopoietin continuous gene fragment.
 PN WO9517205-A1.

PD 29-JUN-1995.
 PA (IMMU-) IMMUNOBIOLOGY RES INST INC.
 Query Match 22.7%; Score 205.8; DB 2; Length 6905;
 Best Local Similarity 83.6%; Pred. No. 2.8e-48;

RESULT 249
 ID ADO13882 standard; DNA; 6905 BP.
 DR Human PRO polynucleotide #720.
 PN WO2004043361-A2.

PD 27-MAY-2004.
 PA (GRTH-) GENTRENTECH INC.
 Query Match 22.7%; Score 205.8; DB 12; Length 6905;
 Best Local Similarity 83.6%; Pred. No. 2.8e-48;

RESULT 250
 ID ACN3728 standard; DNA; 32640 BP.
 DR Human periodontal disease related gene KRT23 SEQ ID NO:138.
 PN WO2004042054-A1.

PD 21-MAY-2004.
 PA (HUBI-) HUBIT GENOMIX INC.

PA (KAMO-) KAMOI K.
 Query Match 22.7%; Score 205.8; DB 13; Length 32640;
 Best Local Similarity 82.4%; Pred. No. 5e-48;

RESULT 251
 ID ACN43878 standard; DNA; 39148 BP.
 DR Human genomic sequence HQC36720.

PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.7%; Score 205.8; DB 11; Length 39148;
 Best Local Similarity 83.6%; Pred. No. 5.4e-48;

RESULT 252
 ID ADA02696 standard; DNA; 59554 BP.
 DR Human TK2 carcinoma associated gene, SEQ ID NO:1214.
 PN WO2003057146-A2.

PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.7%; Score 205.8; DB 9; Length 59554;
 Best Local Similarity 86.3%; Pred. No. 6.3e-48;

RESULT 253
 ID ADB72434 standard; DNA; 59554 BP.
 DR Human TK2 gene.
 PN WO20030583-A2.

PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.7%; Score 205.8; DB 10; Length 59554;
 Best Local Similarity 86.3%; Pred. No. 6.3e-48;

RESULT 254
 ID ADR95944 standard; DNA; 59554 BP.
 DR Human TK2 gene genomic DNA sequence.
 PN WO2003039884-A2.

PD 15-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.7%; Score 205.8; DB 10; Length 59554;
 Best Local Similarity 86.3%; Pred. No. 6.3e-48;

RESULT 255
 ID ABX1034 standard; DNA; 203654 BP.
 DR Human gene encoding calcium channel transporter family member.
 PN US200214238-A1.

PD 03-OCT-2002.
 PA (YANC-) YAN C.

PA (KETC/) KETCHUM K A.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E M.
Query Match 22.7%; Score 205.8; DB 10; Length 203654;
Best Local Similarity 82.7%; Pred. No. 1e-47;
RESULT 256
 ID ASN42054 standard; DNA; 10085 BP.
 DE Genomic sequence #370 encoding novel human enzyme polypeptide.
 PN WO200155301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 205.6; DB 4; Length 10085;
Best Local Similarity 81.7%; Pred. No. 3.6e-48;
RESULT 257
 ID AAL02003 standard; DNA; 10085 BP.
 DE Human reproductuve system related antigen DNA SEQ ID NO: 5491.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 205.6; DB 4; Length 10085;
Best Local Similarity 81.7%; Pred. No. 3.6e-48;
RESULT 258
 ID AAD54634 standard; DNA; 142519 BP.
 DE Human chromodomain helicase DNA binding protein (CHD) encoding DNA #9.
 PN WO200298899-A2.
 PD 12-DEC-2002.
 PA (EXEL-) EXBLIXIS INC.
Query Match 22.7%; Score 205.6; DB 4; Length 10085;
Best Local Similarity 84.4%; Pred. No. 1e-47;
RESULT 259
 ID AAS23041 standard; DNA; 719 BP.
 DE DNA encoding novel bone marrow polypeptide #135.
 PN WO200157187-A2.
 PD 09-AUG-2001.
 PA (NYSE-) HYSEQ INC.
Query Match 22.6%; Score 205.4; DB 4; Length 719;
Best Local Similarity 85.2%; Pred. No. 1.5e-48;
RESULT 260
 ID ABQ72698 standard; cDNA; 2019 BP.
 DE Human MDRT encoding gene, ID NO 250.
 PN WO200247015-A2.
 PD 23-MAY-2002.
 PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.6%; Score 205.4; DB 6; Length 2619;
Best Local Similarity 82.6%; Pred. No. 2.5e-48;
RESULT 261
 ID AAK84729 standard; DNA; 48037 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39541.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 205.4; DB 4; Length 48037;
Best Local Similarity 86.5%; Pred. No. 7.6e-48;
RESULT 262
 ID ASN85983 standard; DNA; 48037 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40795.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 205.4; DB 4; Length 48037;
Best Local Similarity 86.5%; Pred. No. 7.6e-48;
RESULT 263
 ID AAK84730 standard; DNA; 48045 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39542.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 205.4; DB 4; Length 48045;
Best Local Similarity 86.5%; Pred. No. 7.6e-48;
RESULT 264
 ID AAK85984 standard; DNA; 48045 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40796.
 PN WO200157182-A2.

PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 205.4; DB 4; Length 48045;
Best Local Similarity 86.5%; Pred. No. 7.6e-48;
RESULT 265
 ID AZ00870 standard; DNA; 56516 BP.
 DE PGI genomic coding sequence.
 PN WO9912644-A2.
 PD 01-JUL-1999.
 PA (GEST-) GENSET.
Query Match 22.6%; Score 205.4; DB 2; Length 56516;
Best Local Similarity 78.8%; Pred. No. 8.1e-48;
RESULT 266
 ID AZ01022 standard; DNA; 56520 BP.
 DE Wild type PGI coding sequence.
 PN WO9912644-A2.
 PD 01-JUL-1999.
 PA (GEST-) GENSET.
Query Match 22.6%; Score 205.4; DB 2; Length 56520;
Best Local Similarity 78.8%; Pred. No. 8.1e-48;
RESULT 267
 ID ADC8567 standard; DNA; 96593 BP.
 DE Mouse Blm coding sequence.
 PN WO200104520-A2.
 PD 05-JUN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.6%; Score 205.4; DB 10; Length 96593;
Best Local Similarity 83.9%; Pred. No. 9.9e-48;
RESULT 268
 ID ADW2888 standard; DNA; 96594 BP.
 DE Human Blm carcinoma associated gene, SEQ ID NO:1406.
 PN WO200105716-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.6%; Score 205.4; DB 9; Length 96594;
Best Local Similarity 83.9%; Pred. No. 9.9e-48;
RESULT 269
 ID ADW72656 standard; DNA; 96594 BP.
 DE Human Blm gene.
 PN WO20030108582-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.6%; Score 205.4; DB 10; Length 96594;
Best Local Similarity 83.9%; Pred. No. 9.9e-48;
RESULT 270
 ID ADM74493 standard; DNA; 96594 BP.
 DE Human carcinoma associated (CA) nucleic acid #76.
 PN US2004072154-A1.
 PD 15-APR-2004.
 PA (MORR-) MORRIS D W.
 PA (ENGK-) ENGELHARD E K.
Query Match 22.6%; Score 205.4; DB 12; Length 96594;
Best Local Similarity 83.9%; Pred. No. 9.9e-48;
RESULT 271
 ID ADM59536 standard; DNA; 301 BP.
 DE Alu-repeat consensus sequence #2.
 PN WO200302728-A2.
 PD 03-APR-2003.
 PA (BOST-) BOSTON PROBES INC.
Query Match 22.6%; Score 205.2; DB 10; Length 301;
Best Local Similarity 85.8%; Pred. No. 1.2e-48;
RESULT 272
 ID AAK52585 standard; cDNA; 3673 BP.
 DE Human BBD mutant truncated cDNA SEQ ID NO: 3.
 PN WO2003102149-A2.
 PD 11-DEC-2003.
 PA (USH-) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.6%; Score 205.2; DB 12; Length 3673;
Best Local Similarity 81.2%; Pred. No. 3.2e-48;
RESULT 273
 ID AAL52588 standard; cDNA; 3673 BP.
 DE Human BHD mutant truncated cDNA SEQ ID NO: 9.

PN WO2003102149-A2.
 PD 11-DEC-2003.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Query Match 22.6%; Score 205.2; DB 12; Length 3673;
 Best Local Similarity 81.2%; Pred. No. 3.2e-48;
 RESULT 274
 ID AAL52584 Standard; cDNA; 3674 BP.
 DE Human BHD coding sequence.
 PN WO2003102149-A2.
 PD 11-DEC-2003.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Best Local Similarity 22.6%; Score 205.2; DB 12; Length 3674;
 RESULT 275
 ID AAL52589 Standard; cDNA; 3674 BP.
 DE Human BHD mutant truncated cDNA SEQ ID NO: 11.
 PN WO2003102149-A2.
 PD 11-DEC-2003.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Best Local Similarity 22.6%; Score 205.2; DB 12; Length 3674;
 RESULT 276
 ID AAL52587 Standard; cDNA; 3675 BP.
 DE Human BHD mutant truncated cDNA SEQ ID NO: 7.
 PN WO2003102149-A2.
 PD 11-DEC-2003.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Best Local Similarity 22.6%; Score 205.2; DB 12; Length 3675;
 RESULT 277
 ID AAL5616 Standard; DNA; 3676 BP.
 DE Human BHD consensus sequence.
 PN WO2003102149-A2.
 PD 11-DEC-2003.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Best Local Similarity 22.6%; Score 205.2; DB 12; Length 3676;
 RESULT 278
 ID AAL2586 Standard; cDNA; 3702 BP.
 DE Human BHD mutant truncated cDNA SEQ ID NO: 5.
 PN WO2003102149-A2.
 PD 11-DEC-2003.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Best Local Similarity 22.6%; Score 205.2; DB 12; Length 3702;
 RESULT 279
 ID AAK8061 Standard; DNA; 5279 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34873.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.6%; Score 205.2; DB 4; Length 5279;
 Best Local Similarity 83.4%; Pred. No. 3.7e-48;
 RESULT 280
 ID AAK8062 Standard; DNA; 5279 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34874.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity 83.4%; Pred. No. 3.7e-48;
 RESULT 281
 ID AAK8060 Standard; DNA; 5279 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34872.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity 83.4%; Score 205.2; DB 4; Length 5279;
 RESULT 282
 ID AAK8088 Standard; DNA; 17131 BP.
 DE DNA encoding a human geranylgeranyl pyrophosphate synthetase (hGPPS).
 PN WO200005382-A2.

PD 03-FEB-2000.
 PA (GEST) GENSET.
 Query Match 22.6%; Score 205.2; DB 3; Length 17131;
 Best Local Similarity 83.3%; Pred. No. 5.8e-48;
 RESULT 283
 ID AAA3185 Standard; DNA; 32351 BP.
 DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:59.
 PN WO200009525-A2.
 PD 24-FEB-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 Query Match 22.6%; Score 205.2; DB 3; Length 32351;
 Best Local Similarity 77.8%; Pred. No. 7.5e-48;
 RESULT 284
 ID AA21307 Standard; DNA; 32351 BP.
 DE Human low adenosine antisense oligonucleotide related sequence #2874.
 PN WO20062736-A2.
 PD 26-OCT-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 Query Match 22.6%; Score 205.2; DB 3; Length 32351;
 Best Local Similarity 77.8%; Pred. No. 7.5e-48;
 RESULT 285
 ID ABZ97001 Standard; DNA; 32351 BP.
 DE Human nucleic acid sequence.
 PN WO200285308-A2.
 PD 31-OCT-2002.
 PA (EPIG-) EPIGENESIS PHARM INC.
 Query Match 22.6%; Score 205.2; DB 10; Length 32351;
 Best Local Similarity 77.8%; Pred. No. 7.5e-48;
 RESULT 286
 ID ABZ0850 Standard; DNA; 32351 BP.
 DE Human pulmonary and inflammatory target DNA #461.
 PN WO200285309-A2.
 PD 31-OCT-2002.
 PA (EPIG-) EPIGENESIS PHARM INC.
 Query Match 22.6%; Score 205.2; DB 11; Length 32351;
 Best Local Similarity 77.8%; Pred. No. 7.5e-48;
 RESULT 287
 ID AAA3189 Standard; DNA; 40298 BP.
 DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:63.
 PN WO200009525-A2.
 PD 24-FEB-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 Query Match 22.6%; Score 205.2; DB 3; Length 40298;
 Best Local Similarity 77.8%; Pred. No. 8.1e-48;
 RESULT 288
 ID AAF2131 Standard; DNA; 40298 BP.
 DE Human low adenosine antisense oligonucleotide related sequence #2878.
 PN WO200062736-A2.
 PD 26-OCT-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 Query Match 22.6%; Score 205.2; DB 3; Length 40298;
 Best Local Similarity 77.8%; Pred. No. 8.1e-48;
 RESULT 289
 ID ABZ97005 Standard; DNA; 40298 BP.
 DE Human nucleic acid sequence.
 PN WO200285308-A2.
 PD 31-OCT-2002.
 PA (EPIG-) EPIGENESIS PHARM INC.
 Query Match 22.6%; Score 205.2; DB 10; Length 40298;
 Best Local Similarity 77.8%; Pred. No. 8.1e-48;
 RESULT 290
 ID ABD0854 Standard; DNA; 40298 BP.
 DE Human pulmonary and inflammatory target DNA #465.
 PN WO200285309-A2.
 PD 31-OCT-2002.
 PA (EPIG-) EPIGENESIS PHARM INC.
 Query Match 22.6%; Score 205.2; DB 11; Length 40298;
 Best Local Similarity 77.8%; Pred. No. 8.1e-48;
 RESULT 291
 ID ADJ0262 Standard; DNA; 51001 BP.
 DE Human geranylgeranyl diphosphate synthase 1 genomic DNA Seqid 11.

PN US200400550-A1.
 PD 08-JAN-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match Best Local Similarity
 RESULT 292 ID ADL13556 standard; DNA; 95240 BP.
 DB Osteoarthritis-associated polymorphic nucleotide #88.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 293 ID ARK83497 standard; cDNA; 227968 BP.
 DE Human cDNA differentially expressed in granulocytic cells #68.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 294 ID ADQ18338 standard; DNA; 227968 BP.
 DB Human soft tissue sarcoma-upregulated DNA - SEQ ID 1357.
 PN WO200304838-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 295 ID A4Q9281 standard; DNA; 3234 BP.
 DE Human thymopoietin gene fragment.
 PN WO9517205-A1.
 PD 29-JUN-1995.
 PA (IMMU-) IMMUNOBIOLOGY RES INST INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 296 ID AS41738 standard; DNA; 32217 BP.
 DE Genomic sequence #54 encoding novel human enzyme polypeptide.
 PN WO200153301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 297 ID ADU10262 standard; DNA; 51001 BP.
 DE Human geranylgeranyl diphosphate synthase 1 genomic DNA SeqID 11.
 PN US2004005570-A1.
 PD 08-JAN-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 298 ID ADC87336 standard; DNA; 108316 BP.
 DE Human GPCR gene SEQ ID NO:1789.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAD-) NATE INSTITUTE ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED IND SCI & TECHNOLOGY INCUBATOR.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 299 ID AAK86146 standard; DNA; 16997 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40958.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 300 ID AAK86146 standard; DNA; 16997 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40958.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 301 ID AAK80033 standard; DNA; 16997 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34845.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 302 ID ACN4498 standard; DNA; 122614 BP.
 DE Human genomic sequence hcc229191.
 PN WO200373865-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 303 ID ALB0109 standard; DNA; 247582 BP.
 DE Human gene associated with low HDL-C AT3.
 PN US2004043389-A1.
 PD 04-MAR-2004.
 PA (VITI-) VITIVITY INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 304 ID ARK8522 standard; DNA; 2080 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40104.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 305 ID AR45661 standard; DNA; 5970 BP.
 DE Mammary gland bioreactor related DNA #2.
 PN CN1324352-A.
 PD 05-DEC-2001.
 PA (ZHON-) ZHONGLU BIOLOGICAL ENG CO LTD SHANGHAI.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 306 ID AR43493 standard; DNA; 6870 BP.
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2522.
 PN WO200009525-A2.
 PD 24-FEB-2000.
 PA (UNIV-) UNIV EAST CAROLINA.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 307 ID AR20955 standard; DNA; 6870 BP.
 DE Interleukin-11 polynucleotide fragment #2522.
 PN WO200062736-A2.
 PD 26-OCT-2000.
 PA (UNIV-) UNIV EAST CAROLINA.
 PA (NYCE-) NYCE J W.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 308 ID AB296649 standard; DNA; 6870 BP.
 DE Human interleukin-11 nucleic acid.
 PN WO20028308-A2.
 PD 31-OCT-2002.
 PA (EPIC-) EPIGENESIS PHARM INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 309 ID ABD19514 standard; DNA; 6870 BP.
 DE Human interleukin-11 DNA fragment #3.
 PN WO20028309-A2.
 PD 31-OCT-2002.
 PA (EPIC-) EPIGENESIS PHARM INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 310 ID ABD19514 standard; DNA; 6870 BP.

RESULT 310
ID AAA34834 standard; DNA; 8055 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2523.
PN WO200009528-A2.
PD 24-FEB-2000.

RESULT 311
ID AAF20556 standard; DNA; 8055 BP.
DE Interleukin-11 polynucleotide fragment #2523.
PN WO2000052736-A2.
PD 26-OCT-2000.

PA (UYEC-) UNIV EAST CAROLINA.
Query Match Best Local Similarity 81.4%; Pred. No. 7.4e-48;

PA (NYCB-) NYCC J W.
Query Match Best Local Similarity 81.4%; Score 204.4; DB 3; Length 8055;
ID ABZ96550 standard; DNA; 8055 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.

PA (EPIC-) EPIGENESIS PHARM INC.
Query Match Best Local Similarity 81.4%; Score 204.4; DB 10; Length 8055;
Best Local Similarity 81.4%; Pred. No. 7.4e-48;

RESULT 313
ID ABD19512 standard; DNA; 8055 BP.
DE Human interleukin-11 DNA fragment #1.
PN WO200285308-A2.
PD 31-OCT-2002.

PA (EPIC-) EPIGENESIS PHARM INC.
Query Match Best Local Similarity 81.4%; Score 204.4; DB 11; Length 8055;
Best Local Similarity 81.4%; Pred. No. 7.4e-48;

RESULT 314
ID AAK87584 standard; DNA; 1417 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42396.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match Best Local Similarity 82.7%; Score 204.4; DB 4; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 315
ID AAK71816 standard; DNA; 1417 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26628.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match Best Local Similarity 82.7%; Score 204.4; DB 4; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 316
ID AAK71113 standard; DNA; 1417 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27925.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match Best Local Similarity 82.7%; Score 204.4; DB 4; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 317
ID AAK162923 standard; DNA; 14417 BP.
DE Human genomic DNA SEQ ID NO 251.
PN WO200155449-A1.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match Best Local Similarity 82.7%; Score 204.4; DB 4; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 318
ID ABZ74674 standard; DNA; 1417 BP.
DE Secreted protein gene 391 genomic fragment HB8FC45, SEQ ID NO:1820.
PN WO200277013-A2.
PD 03-OCT-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match Best Local Similarity 82.7%; Score 204.4; DB 4; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 319
ID ABZ68196 standard; DNA; 14417 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1719.
PN WO20037186-A2.
PD 03-OCT-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 320
ID AAK73099 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27911.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 321
ID AAK8568 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42380.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match Best Local Similarity 82.7%; Score 204.4; DB 4; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 322
ID AAK8590 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40102.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match Best Local Similarity 82.7%; Score 204.4; DB 4; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 323
ID AAK71814 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26626.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match Best Local Similarity 82.7%; Score 204.4; DB 4; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 324
ID AA162921 standard; DNA; 14426 BP.
DE Human genomic DNA SEQ ID NO 249.
PN WO200155449-A1.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match Best Local Similarity 82.7%; Score 204.4; DB 4; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 325
ID ABZ74673 standard; DNA; 14426 BP.
DE Secreted protein gene 391 genomic fragment HB8FC45, SEQ ID NO:1820.
PN WO200277013-A2.
PD 03-OCT-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match Best Local Similarity 82.7%; Score 204.4; DB 8; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 326
ID ABZ68195 standard; DNA; 14426 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1718.
PN WO200277186-A2.
PD 03-OCT-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match Best Local Similarity 82.7%; Score 204.4; DB 10; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 327
ID ABD34665 standard; DNA; 112453 BP.
DE Human cancer-associated genomic DNA HD13-070.
PN WO2004074320-A2.
PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
Query Match Best Local Similarity 83.9%; Score 204.4; DB 13; Length 112453;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 328

ID ADQ59167 standard; DNA; 120670 BP.
 DE NSI-H carcinoma genomic DNA sequence SEQ ID NO:4.
 PN KR2004008012-A.
 PD 28-JAN-2004;
 PA (KIMH-) KIM H G.
 PA (KIMN-) KIM N G.
 PA (LEJ-) LEE J S.
 PA (RHEB-) RHEB H S.

Query Match Best Local Similarity 22.5%; Score 204.4; DB 12; Length 120670;
 RESULT 329
 ID ADE82948 standard; DNA; 167163 BP.
 DE Human PVT1 genomic DNA sequence.
 PN WO2003080808-A2.
 PD 02-OCT-2003;

PA (ISAGR-) SAGRES DISCOVERY Query Match Best Local Similarity 84.1%; Pred. No. 2.1e-47;
 RESULT 329
 ID ADE82948 standard; DNA; 167163 BP.
 DE Human PVT1 genomic DNA sequence.
 PN WO2003080808-A2.

PA (UYEC-) UNIV EAST CAROLINA Query Match Best Local Similarity 81.4%; Pred. No. 2.4e-47;
 RESULT 330
 ID AAF21437 standard; DNA; 209273 BP.
 DE Human factor-related antisense polynucleotide #3004.
 PN WO20062735-A2.
 PD 26-OCT-2006.

PA (UYEC-) UNIV EAST CAROLINA Query Match Best Local Similarity 81.4%; Pred. No. 2.6e-47;
 RESULT 331
 ID ABZ97131 standard; DNA; 209274 BP.
 DE Human enzyme-related antisense polynucleotide.
 PN WO200205309-A2.
 PD 31-OCT-2002.

PA (BPIG-) BPIGENESIS PHARM INC. Query Match Best Local Similarity 81.4%; Pred. No. 2.6e-47;
 RESULT 332
 ID ABD17970 standard; DNA; 209284 BP.
 DE Human factor-related antisense polynucleotide.
 PN WO200205309-A2.

PA (BPIG-) BPIGENESIS PHARM INC. Query Match Best Local Similarity 81.4%; Pred. No. 2.6e-47;
 RESULT 333
 ID ABZ96807 standard; cDNA; 1777 BP.
 DE Human uteroglobin 9-encoding cDNA.
 PN WO200198337-A1.
 PD 27-DEC-2001.

PA (GHAN-) SHANGHAI BIOWINDOW GENE DEV INC. Query Match Best Local Similarity 81.4%; Pred. No. 2.6e-47;
 RESULT 334
 ID ARG69133 standard; DNA; 4736 BP.
 DE Human ABC1 gene exon 2.
 PN WO20055318-A2.
 PD 21-SEP-2000.

PA (UYBR-) UNIV BRITISH COLUMBIA. Query Match Best Local Similarity 80.9%; Pred. No. 4.7e-48;
 RESULT 334
 ID ARG69133 standard; DNA; 4736 BP.

PA (XENO-) XENON BIORESEARCH INC. Query Match Best Local Similarity 80.7%; Pred. No. 6.9e-48;
 RESULT 335
 ID ARS04033 standard; DNA; 11754 BP.
 DE Human ABC1 gene, partial genomic clone #1.
 PN WO20010848-A2.
 PD 03-MAY-2001.

PA (AVET-) AVENTIS PHARMA SA. Query Match Best Local Similarity 22.5%; Score 204.2; DB 4; Length 11754;
 RESULT 335
 ID ARS04033 standard; DNA; 11754 BP.
 DE Best local similarity 80.7%; Pred. No. 9.8e-48;
 RESULT 336
 ID AB158149 standard; DNA; 11754 BP.
 DE Human ABC1 transporter gene fragment #3.
 PN WO200236770-A2.
 PD 10-MAY-2002.

PA (AVET-) AVENTIS PHARMA SA. Query Match Best Local Similarity 22.5%; Score 204.2; DB 6; Length 11754;
 PA (INRM-) INSERM INST NAT SANTE & RECH MEDICALE. Query Match Best Local Similarity 22.5%; Score 204.2; DB 6; Length 11754;
 PA (INRM-) INSERM INST NAT SANTE & RECH MEDICALE. Query Match Best Local Similarity 80.7%; Pred. No. 9.8e-48;
 RESULT 337
 ID ADP65433 standard; DNA; 149034 BP.
 DE Human ABC1 (ABC1) gene, complete cds DNA.
 PN WO2003072827-A1.
 PD 04-SEP-2003.

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT. Query Match Best Local Similarity 22.5%; Score 204.2; DB 11; Length 149034;
 PA (UYBR-) UNIV BRITISH COLUMBIA. Query Match Best Local Similarity 80.7%; Pred. No. 2.6e-47;
 RESULT 338
 ID AAF92031 standard; DNA; 183999 BP.
 DE Human ABC1 genomic DNA.
 PN WO200115676-A2.

PA (UYBR-) UNIV BRITISH COLUMBIA. Query Match Best Local Similarity 80.7%; Pred. No. 2.6e-47;
 RESULT 338
 ID AAF92031 standard; DNA; 183999 BP.
 DE Human ABC1 genomic DNA.

PA (XENO-) XENON GENETICS INC. Query Match Best Local Similarity 80.7%; Pred. No. 2.8e-47;
 RESULT 339
 ID AAL04782 standard; DNA; 22927 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 7470.
 PN WO200153320-A2.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match Best Local Similarity 81.6%; Pred. No. 1.4e-47;
 RESULT 340
 ID ABU197677 standard; DNA; 22927 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2329.
 PN WO200155317-A2.
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match Best Local Similarity 81.6%; Pred. No. 1.4e-47;
 RESULT 341
 ID ADC86460 standard; DNA; 33137 BP.
 DE Human GPCR gene SEQ ID NO:913.
 PN EP1270724-A2.

PA (NRAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. Query Match Best Local Similarity 81.6%; Pred. No. 1.4e-47;
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO. Query Match Best Local Similarity 82.5%; Score 204; DB 10; Length 33137;

PA (NRAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. Query Match Best Local Similarity 84.1%; Pred. No. 1.7e-47;
 RESULT 342
 ID ACT04345 standard; DNA; 48840 BP.
 DE Genomic DNA encoding human latrophilin 1 (LPH1).
 PN US2003054347-A1.
 PD 20-MAR-2003.

PA (UNMI-) UNIV MICHIGAN. Query Match Best Local Similarity 84.1%; Pred. No. 1.9e-47;
 RESULT 343
 ID ASK48904 standard; DNA; 3635 BP.
 DE Novel human kallikrein KUK15, intron 1.
 PN WO20024485-A2.
 PD 21-FEB-2002.

PA (MOUN-) MOUNT SINAI HOSPITAL. Query Match Best Local Similarity 22.5%; Score 203.8; DB 6; Length 3635;
 PA (MOUN-) MOUNT SINAI HOSPITAL. Query Match Best Local Similarity 86.2%; Pred. No. 8.1e-48;
 RESULT 344
 ID ABK48346 standard; DNA; 8735 BP.
 DE Genomic DNA encoding novel human kallikrein KUK15.
 PN WO20024485-A2.
 PD 21-FEB-2002.

PA (MOUN-) MOUNT SINAI HOSPITAL. Query Match Best Local Similarity 22.5%; Score 203.8; DB 6; Length 3635;
 PA (MOUN-) MOUNT SINAI HOSPITAL. Query Match Best Local Similarity 86.2%; Pred. No. 8.1e-48;
 RESULT 345
 ID ADM10936 standard; DNA; 8735 BP.
 DE Human kallikrein 15 gene, marker of endocrine cancer.

PN WO2004029285-A2.
 PD 08-APR-2004.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Query Match Similarity 22.5%; Score 203.8; DB 12; Length 8735;
 Best Local Similarity 86.2%; Pred. No. 1.1e-47;
 RESULT 346
 ID AUS34456 Standard; DNA; 16640 BP.
 DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1670.
 PN WO2004083403-A2.
 PD 30-SEP-2004.
 PA (APPL-) APPLERA CORP. 22.5%; Score 203.8; DB 13; Length 16640;
 Best Local Similarity 86.2%; Pred. No. 1.5e-47;
 RESULT 347
 ID ADB34479 Standard; DNA; 18235 BP.
 DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1693.
 PN WO2004083403-A2.
 DR Human VDAC1 Carcinoma associated gene, SEQ ID NO:1232.
 PA (SAGR-) SAGRES DISCOVERY.
 Best Local Similarity 79.5%; Score 203.8; DB 9; Length 53413;
 RESULT 348
 ID ADB72452 Standard; DNA; 53413 BP.
 DE Human VDAC1 gene.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY. 22.5%; Score 203.8; DB 10; Length 53413;
 Best Local Similarity 79.5%; Pred. No. 2.3e-47;
 RESULT 349
 ID ADR95962 Standard; DNA; 53413 BP.
 DE Human VDAC1 gene genomic DNA Sequence.
 PN WO2003039484-A2.
 PD 15-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY. 22.5%; Score 203.8; DB 10; Length 53413;
 Best Local Similarity 79.5%; Pred. No. 2.3e-47;
 RESULT 350
 ID AAK77913 Standard; DNA; 644 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32725.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (HUMA-) HUMAN GENOME SCI INC. 22.4%; Score 203.6; DB 10; Length 93390;
 Best Local Similarity 81.6%; Pred. No. 1.7e-47;
 RESULT 351
 ID AAK77915 Standard; DNA; 646 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32727.
 PN WO2003057182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. 22.4%; Score 203.4; DB 4; Length 646;
 Best Local Similarity 83.7%; Pred. No. 5.4e-48;
 RESULT 352
 ID AA184724 Standard; cDNA; 777 BP.
 DE Human Polynucleotide SEQ ID NO 4784.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSS-) HYSEQ INC. 22.4%; Score 203.4; DB 4; Length 646;
 Best Local Similarity 83.7%; Pred. No. 5.4e-48;
 RESULT 353
 ID ACN35520 Standard; cDNA; 2068 BP.
 DE Tumour-associated antigenic target (TAT) cDNA DNA325729, SEQ ID NO:3715.
 PN WO200403015-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC. 22.4%; Score 203.4; DB 4; Length 777;
 Best Local Similarity 79.7%; Pred. No. 5.8e-48;
 RESULT 354
 ID AAK77914 Standard; cDNA; 2558 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32726.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. 22.4%; Score 203.4; DB 4; Length 2558;
 Best Local Similarity 83.7%; Pred. No. 9.2e-48;
 RESULT 355
 ID AAL0534 Standard; DNA; 4067 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 7222.
 PN WO20015310-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. 22.4%; Score 203.4; DB 4; Length 4067;
 Best Local Similarity 79.1%; Pred. No. 1.1e-47;
 RESULT 356
 ID AAL0537 Standard; DNA; 4067 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 7225.
 PN WO20015310-A2.
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 203.4; DB 4; Length 4067; Best Local Similarity 79.1%; Pred. No. 1.1e-47; RESULT 364 ID ABL97457 standard; DNA; 4067 BP. DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2109. PN WO200155317-A2.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 203.4; DB 4; Length 4067; Best Local Similarity 79.1%; Pred. No. 1.1e-47; RESULT 365 ID ABL97460 standard; DNA; 4067 BP. DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2112. PN WO200155317-A2.

PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 203.4; DB 4; Length 4067; Best Local Similarity 79.1%; Pred. No. 1.1e-47; RESULT 366 ID AAK77916 standard; DNA; 7759 BP. DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32728. PN WO200157182-A2.

PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 203.4; DB 4; Length 7759; Best Local Similarity 83.7%; Pred. No. 1.4e-47; RESULT 367 ID AAK73223 standard; DNA; 31051 BP. DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28035. PN WO200157182-A2.

PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 203.4; DB 4; Length 31051; Best Local Similarity 77.9%; Pred. No. 2.4e-47; RESULT 368 ID AAK89112 standard; DNA; 32190 BP. DE Human digestive system antigen genomic sequence SEQ ID NO: 2688. PN WO200155314-A2.

PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 203.4; DB 4; Length 32190; Best Local Similarity 83.7%; Pred. No. 2.4e-47; RESULT 369 ID AAK31862 standard; DNA; 32190 BP. DE Human liver associated genomic DNA #36. PN WO200155335-A1.

PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 203.4; DB 5; Length 32190; Best Local Similarity 83.7%; Pred. No. 2.4e-47; RESULT 370 ID ABN90217 standard; DNA; 32190 BP. DE Human liver antigen HFLSJ61 genomic sequence, SEQ ID NO:338. PN US2002042096-A1.

PD 11-APR-2002. PA (ROSE/) ROSEN C A. PA (RUBE/) RUBEN S M. PA (BARA/) BARASH S C. Query Match 22.4%; Score 203.4; DB 6; Length 32190; Best Local Similarity 83.7%; Pred. No. 2.4e-47; RESULT 371 ID ABL15130 standard; DNA; 32190 BP. DE Human liver-related genomic DNA - SEQ ID 338. PN US2003077602-A1.

PD 24-APR-2003. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 203.4; DB 11; Length 194803; Best Local Similarity 75.1%; Pred. No. 5.6e-47; RESULT 372 ID ABB69895 standard; DNA; 56737 BP. DE Human hypoxanthine-guanine phosphoribosyltransferase (HPRT) gene. PN US2002102731-A1.

PD 01-AUG-2002. PA (UTNY) UNTV NEW YORK STATE RESS FOUND. Query Match 22.4%; Score 203.4; DB 6; Length 56737; Best Local Similarity 83.8%; Pred. No. 3e-47; RESULT 373 ID AD08126 standard; DNA; 191395 BP. DE Human gene associated with low HDL-C PA12. PN US200404389-A1.

PD 04-MAR-2004. PA (VITI-) VIRTIVITY INC. Query Match 22.4%; Score 203.4; DB 12; Length 191395; Best Local Similarity 83.8%; Pred. No. 4.9e-47; RESULT 374 ID ABD32868 standard; DNA; 238417 BP. DE Human cancer-associated genomic DNA HD17-053. PN WO2004074320-A2.

PD 02-SEP-2004. PA (SAGR-) SAGRES DISCOVERY INC. Query Match 22.4%; Score 203.4; DB 13; Length 238417; Best Local Similarity 83.8%; Pred. No. 5.3e-47; RESULT 375 ID ABV74806 standard; cDNA; 2009 BP. DE Signalase 11.22 coding sequence. PN CN1345931-A.

PD 24-APR-2002. PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC. Query Match 22.4%; Score 203.4; DB 6; Length 2009; Best Local Similarity 83.0%; Pred. No. 9.6e-48; RESULT 376 ID ABR97867 standard; DNA; 13161 BP. DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:81. PN WO200116311-A1.

PD 08-MAR-2001. PA (HISM) HISAMITSU PHARM CO LTD. PA (CHIB-) CHIBA PREFECTURE. Query Match 22.4%; Score 203.4; DB 5; Length 13161; Best Local Similarity 83.3%; Pred. No. 2e-47; RESULT 377 ID AAK78275 standard; DNA; 35959 BP. DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33087. PN WO200157182-A2.

PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 203.2; DB 4; Length 35959; Best Local Similarity 78.7%; Pred. No. 2.9e-47; RESULT 378 ID ADL13830 standard; DNA; 10550 BP. DE Osteoarthritis-associated polymorphic nucleotide #382. PN WO2003054166-A2.

PD 03-JUL-2003. PA (INCY-) INCYTB GENOMICS INC. Query Match 22.4%; Score 203.2; DB 10; Length 180550; Best Local Similarity 81.8%; Pred. No. 5.4e-47; RESULT 379 ID ACM44398 standard; DNA; 194883 BP. DE Human genomic sequence hCG20056. PN WO2003173826-A2.

PD 12-SEP-2003. PA (SAGR-) SAGRES DISCOVERY. Query Match 22.4%; Score 203.2; DB 11; Length 194803; Best Local Similarity 75.1%; Pred. No. 5.6e-47; RESULT 380 ID AD33276 standard; DNA; 255190 BP. DE Human cancer-associated (CA) gene HD07-048. PN WO20040458146-A2.

PD 15-JUL-2004. PA (SAGR-) SAGRES DISCOVERY INC. Query Match 22.4%; Score 203.2; DB 13; Length 256190; Best Local Similarity 83.3%; Pred. No. 6.2e-47; RESULT 381 ID AAK80969 standard; DNA; 6187 BP. DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35781. PN WO200157182-A2.

PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 203; DB 4; Length 6187; Best Local Similarity 81.7%; Pred. No. 1.7e-47; RESULT 382.

ID AAB9631 standard; DNA; 99014 BP. DE Gene #3429 used to diagnose liver cancer. PN WO200229103-A2.

PD 14-APR-2002. PA (GENE-) GENE LOGIC INC. Query Match 22.4%; Score 203; DB 6; Length 99014; Best Local Similarity 76.4%; Pred. No. 4.9e-47; RESULT 383.

ID AAD08215 standard; DNA; 114793 BP. DE Human genome from BAC clone, hbm168. PN WO200142434-A1.

PD 14-JUN-2001. PA (MERL.) MERCK & CO INC. Query Match 22.4%; Score 203; DB 4; Length 114793; Best Local Similarity 84.1%; Pred. No. 5.2e-47; RESULT 384.

ID ACN44170 standard; DNA; 196686 BP. DE Human genomic sequence hCG39530. PN WO2001073825-A2.

PD 12-SEP-2003. PA (SAGR-) SAGRES DISCOVERY. Query Match 22.4%; Score 203; DB 11; Length 196686; Best Local Similarity 83.7%; Pred. No. 6.4e-47; RESULT 385.

ID ADQ97523 standard; DNA; 215974 BP. DE Human cancer associated Sequence HD09-008, SEQ ID 500. PN WO2004063034-A2.

PD 22-JUN-2004. PA (SAGR-) SAGRES DISCOVERY INC. Query Match 22.4%; Score 203; DB 12; Length 215974; Best Local Similarity 81.7%; Pred. No. 6.6e-47; RESULT 386.

ID AAD04910 standard; cDNA; 2013 BP. DE Human secreted protein-encoding gene 4 cDNA clone HSLH186, SEQ ID NO:23. PN WO20134799-A1.

PD 17-MAY-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 202.8; DB 4; Length 2013; Best Local Similarity 74.0%; Pred. No. 1.3e-47; RESULT 387.

ID AAK05936 standard; DNA; 3753 BP. DE Human reproductive system related antigen DNA SEQ ID NO: 7624. PN WO200155330-A2.

PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 202.8; DB 4; Length 3753; Best Local Similarity 79.2%; Pred. No. 1.6e-47; RESULT 388.

ID ABL97830 standard; DNA; 3753 BP. DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2482. PN WO200155317-A2.

PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 202.8; DB 4; Length 3753; Best Local Similarity 79.2%; Pred. No. 1.6e-47; RESULT 389.

ID AAD04901 standard; cDNA; 3781 BP. DE Human secreted protein-encoding gene 4 cDNA clone HSLH186, SEQ ID NO:14. PN WO200134799-A1.

PD 17-MAY-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 202.8; DB 4; Length 3781; Best Local Similarity 74.0%; Pred. No. 1.6e-47; RESULT 390.

ID AAK71815 standard; DNA; 14448 BP. DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:42392. PN WO200157182-A2.

PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 202.8; DB 4; Length 14448; Best Local Similarity 82.4%; Pred. No. 2.7e-47; RESULT 391.

ID AAK73111 standard; DNA; 14448 BP. DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:27923. PN WO200157182-A2.

PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 202.8; DB 4; Length 14448; Best Local Similarity 82.4%; Pred. No. 2.7e-47; RESULT 392.

ID AAK73111 standard; DNA; 14448 BP. DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:27923. PN WO200157182-A2.

PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 202.8; DB 4; Length 14448; Best Local Similarity 82.4%; Pred. No. 2.7e-47; RESULT 393.

ID AA162922 standard; DNA; 14448 BP. DE Human genomic DNA SEQ ID NO 250. PN WO200155419-A1.

PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 202.8; DB 4; Length 14448; Best Local Similarity 82.4%; Pred. No. 2.7e-47; RESULT 394.

ID AA162922 standard; DNA; 14448 BP. DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:27928. PN WO200157182-A2.

PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 202.8; DB 4; Length 14451; Best Local Similarity 82.4%; Pred. No. 2.7e-47; RESULT 395.

ID AA71818 standard; DNA; 14451 BP. DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:26630. PN WO200157182-A2.

PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 202.8; DB 4; Length 14451; Best Local Similarity 82.4%; Pred. No. 2.7e-47; RESULT 396.

ID AAK87587 standard; DNA; 14451 BP. DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:42399. PN WO200157182-A2.

PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 202.8; DB 4; Length 14451; Best Local Similarity 82.4%; Pred. No. 2.7e-47; RESULT 397.

ID AAI62925 standard; DNA; 14451 BP. DE Human genomic DNA SEQ ID NO 253. PN WO200155419-A1.

PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 202.8; DB 4; Length 14451; Best Local Similarity 82.4%; Pred. No. 2.7e-47; RESULT 398.

ID AAL03917 standard; DNA; 22299 BP. DE Human reproductive system related antigen DNA SEQ ID NO: 6605. PN WO200155330-A2.

PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.4%; Score 202.8; DB 4; Length 22299; Best Local Similarity 83.6%; Pred. No. 3.2e-47; RESULT 399.

ID AAS40117 standard; DNA; 22299 BP. DE DNA encoding human prostate cancer antigen, seq ID NO 469. PN WO200155316-A2.

PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC.

Query Match	22.4%	Score 202.8;	DB 5;	Length 22299;	ID ACN45054 standard; DNA; 133632 BP.
Best Local Similarity	83.6%	Pred. No. 3.2e-47;			DE Human genomic sequence hcg28560.
RESULT 400					PN WO2003073826-A2.
ID ADJ0523 standard; DNA; 22299 BP.					PD 12-SEP-2003.
DE Human probestate cancer associated gene-related DNA seqID469.					PA (SAGR-) SAGRES DISCOVERY.
PN US2003054313-A1.					Query Match 22.4%; Score 202.8; DB 11; Length 133632;
PD 20-MAR-2003.					DE Best Local Similarity 76.0%; Pred. No. 6.3e-47;
DB (HUMA-) HUMAN GENOME SCI INC.					ID ADC56769 standard; DNA; 1051 BP.
Query Match 22.4%; Score 202.8; DB 11; Length 22299;					DE DNA (SeqID 4) related to the human thymidylic acid synthetase gene.
Best Local Similarity 83.6%; Pred. No. 3.2e-47;					PN JP2003102480-A.
RESULT 401					PD 08-APR-2003.
ID ADM9721 standard; DNA; 28865 BP.					PA (SRLS-) SRL KK.
DE prostate and breast cancer associated human gene CYP17.					Query Match 22.3%; Score 202.6; DB 10; Length 1051;
PN WO2004028366-A2.					DE Best Local Similarity 81.7%; Pred. No. 1.1e-47;
PD 08-APR-2004.					ID AAS34702 standard; DNA; 3147 BP.
PA (AMSH-) AMERSHAM BIOSCIENCES SV CORP.					DE Human DNA for a novel footail antigen, SEQ ID No 2126.
Query Match 22.4%; Score 202.8; DB 12; Length 26865;					PN WO200155312-A2.
Best Local Similarity 78.9%; Pred. No. 3.4e-47;					PD 02-AUG-2001.
RESULT 402					PA (HUMA-) HUMAN GENOME SCI INC.
ID ADD5001 standard; DNA; 27067 BP.					Query Match 22.3%; Score 202.6; DB 5; Length 3147;
DE Human secreted protein encoding gene.					DE Best Local Similarity 83.1%; Pred. No. 1.7e-47;
Query Match 22.4%; Score 202.8; DB 10; Length 27067;					ID AAF75338 standard; cDNA; 3200 BP.
Best Local Similarity 83.6%; Pred. No. 3.4e-47;					DE Human TGF-beta receptor cDNA clone HDPGX45.
RESULT 403					PN WO200112670-A1.
ID AA35003 standard; DNA; 56583 BP.					PD 22-FEB-2001.
DE Human adenosine receptor related sequence SEQ ID NO:2692.					PA (HUMA-) HUMAN GENOME SCI INC.
PN WO200009525-A2.					Query Match 22.3%; Score 202.6; DB 4; Length 3200;
PD 24-FEB-2000.					DE Best Local Similarity 81.7%; Pred. No. 1.7e-47;
PA (UYEC-) UNTIV EAST CAROLINA.					ID ABK14000 standard; cDNA; 3353 BP.
Query Match 22.4%; Score 202.8; DB 3; Length 56583;					DE CDNA encoding human protein kinase 3700.
Best Local Similarity 83.4%; Pred. No. 4.5e-47;					PN WO200224921-A2.
RESULT 404					PD 28-MAR-2002.
ID AAF21125 standard; DNA; 56583 BP.					PA (MILL-) MILLENIUM PHARM INC.
DE Human low adenosine antisense oligonucleotide related sequence #2692.					Query Match 22.3%; Score 202.6; DB 6; Length 3353;
PN WO200067376-A2.					DE Best Local Similarity 81.7%; Pred. No. 1.7e-47;
PD 26-OCT-2000.					ID AAF1410 standard; cDNA; 3353 BP.
PA (NICE/-) NYCE J W.					DE Novel human gene 3700 cDNA.
Query Match 22.4%; Score 202.8; DB 3; Length 56583;					PN US2004058355-A1.
Best Local Similarity 83.4%; Pred. No. 4.5e-47;					PD 25-MAR-2004.
RESULT 405					PA (MILL-) MILLENIUM PHARM INC.
ID AD296819 standard; DNA; 56583 BP.					Query Match 22.3%; Score 202.6; DB 12; Length 3353;
DE Human nucleic acid sequence.					DE Best Local Similarity 81.7%; Pred. No. 1.7e-47;
PN WO200285308-A2.					ID AAF26459 standard; cDNA; 3360 BP.
PD 31-OCT-2002.					DE Human kinase PKIN-12 cDNA.
PA (EPICG-) EPIGENESIS PHARM INC.					PN WO200195547-A2.
Query Match 22.4%; Score 202.8; DB 10; Length 56583;					PD 20-DEC-2001.
Best Local Similarity 83.4%; Pred. No. 4.5e-47;					PA (INCY-) INCYTE GENOMICS INC.
RESULT 406					Query Match 22.3%; Score 202.6; DB 6; Length 3360;
ID ABD20668 standard; DNA; 56583 BP.					DE Best Local Similarity 81.7%; Pred. No. 1.7e-47;
DE Human pulmonary and inflammatory target DNA #279.					ID AAF26459 standard; cDNA; 3360 BP.
PN WO200253039-A2.					DE Human full-length cDNA, SEQ ID NO: 2918.
PD 31-OCT-2002.					ID EP1130094-A2.
PA (BETG-) EPIGENESIS PHARM INC.					PN 05-SEP-2001.
Query Match 22.4%; Score 202.8; DB 11; Length 56583;					PA (HBLI-) HELIX RES INST.
Best Local Similarity 83.4%; Pred. No. 4.5e-47;					Query Match 22.3%; Score 202.6; DB 4; Length 3395;
RESULT 407					DE Best Local Similarity 81.7%; Pred. No. 1.7e-47;
ID ACTN44056 standard; DNA; 99886 BP.					ID AAK9420 standard; cDNA; 3395 BP.
DE Human genomic sequence hcg5674.					DE Full-length human cDNA clone SeqID 2918.
PN WO2003073826-A2.					DE Full-length human cDNA clone SeqID 2918.
PD 12-SEP-2003.					PN EP1396543-A2.
PA (SAGR-) SGRES DISCOVERY.					PD 10-MAR-2004.
Query Match 22.4%; Score 202.8; DB 11; Length 99886;					PA (RBAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity 79.2%; Pred. No. 5.6e-47;					Query Match 22.3%; Score 202.6; DB 12; Length 3395;
RESULT 408					DE Best Local Similarity 81.7%; Pred. No. 1.7e-47;
ID ADD17329 standard; DNA; 101685 BP.					ID ADU30815 standard; cDNA; 3395 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 146.					DE Full-length human cDNA clone SeqID 2918.
PN WO2004048938-A2.					DE Full-length human cDNA clone SeqID 2918.
PD 10-JUN-2004.					PN EP1396543-A2.
PA (PROT-) PROTEIN DESIGN LABS INC.					PD 08-APR-2004.
Query Match 22.4%; Score 202.8; DB 12; Length 101685;					PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity 79.2%; Pred. No. 5.7e-47;					Query Match 22.3%; Score 202.6; DB 12; Length 3395;
RESULT 409					DE Best Local Similarity 81.7%; Pred. No. 1.7e-47;
ID ABX71420 standard; cDNA; 3443 BP.					ID ABX71420 standard; cDNA; 3443 BP.

DE Human cell cycle-associated cDNA from clone DKFZphtes3_7j3.
 PN WO200112659-A2.
 PD 22-FEB-2001.
 ID ADB769 standard; DNA; 3443 BP.
 DE (GERU-) GERMAN HUMAN GENOME PROJECT.
 DR Novel human secreted and transmembrane protein cDNA SeqID 639.
 PN WO2005072035-A2.
 PD 04-SEP-2003.
 PA (GEBH-) GENENTECH INC.
 Query Match Best Local Similarity 81.7%; Score 202.6; DB 10; Length 3443;
 Best Local Similarity 81.7%; Pred. No. 1.8e-47;
 RESULT 420
 ID ADP81952 standard; cDNA; 3443 BP.
 DE Leukaemia-related DNA sequence #2508.
 PN WO2003039443-A2.
 PD 15-MAR-2003.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 DR (UYLU-) UNIV LUDWIG MAXIMILIANS.
 PA (HAFE-) HABERLACH T.
 PA (SCHO-) SCHIOCH C.
 PA (KERN-) KERN W.
 Query Match Best Local Similarity 81.7%; Score 202.6; DB 10; Length 3443;
 Best Local Similarity 81.7%; Pred. No. 1.8e-47;
 RESULT 421
 ID ADP20171 standard; cDNA; 3443 BP.
 DE Human PRO polyynucleotide #540.
 PN WO2004043351-A2.
 PD 27-MAY-2004.
 PA (GEBH-) GENENTECH INC.
 Query Match Best Local Similarity 81.7%; Score 202.6; DB 12; Length 3443;
 Best Local Similarity 81.7%; Pred. No. 1.8e-47;
 RESULT 422
 ID AAK68379 standard; DNA; 4646 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23791.
 PN WO200517182-A2.
 PD 09-AUG-2005.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 82.3%; Score 202.6; DB 4; Length 4646;
 Best Local Similarity 82.9%; Pred. No. 2e-47;
 RESULT 423
 ID ABA20357 standard; DNA; 11585 BP.
 DE Human nervous system related polyynucleotide SEQ ID NO 12688.
 PN WO201505963-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 82.3%; Score 202.6; DB 5; Length 11585;
 Best Local Similarity 83.3%; Pred. No. 2.8e-47;
 RESULT 424
 ID AAS36927 standard; DNA; 20869 BP.
 DE Human cardiovascular system antigen genomic DNA SEQ ID No 2427.
 PN WO200553321-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 82.3%; Score 202.6; DB 5; Length 20869;
 Best Local Similarity 85.6%; Pred. No. 3.5e-47;
 RESULT 425
 ID AAK85001 standard; DNA; 20869 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39813.
 PN WO2005157182-A2.
 PD 09-AUG-2005.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 82.3%; Score 202.6; DB 4; Length 20869;
 Best Local Similarity 85.6%; Pred. No. 3.5e-47;
 RESULT 426
 ID ABA16245 standard; DNA; 20869 BP.
 DE Human nervous system related polyynucleotide SEQ ID NO 8576.
 PN WO2005150963-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 82.3%; Score 202.6; DB 5; Length 20869;

Best Local Similarity 85.6%; Pred. No. 3.5e-47;
 RESULT 427
 ID ADB4721 standard; DNA; 20869 BP.
 DE Human cardiovascular system related genomic DNA #1187.
 PN US2003059908-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 85.6%; Pred. No. 3.5e-47;
 RESULT 428
 ID ADJ09039 standard; DNA; 20869 BP.
 DE Human cardiovascular system associated polypeptide-related DNA SeqID2427.
 PN US2004005555-A1.
 PD 08-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 85.6%; Pred. No. 3.5e-47;
 RESULT 429
 ID AAK82338 standard; DNA; 48908 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37150.
 PN WO200517182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 81.7%; Score 202.6; DB 4; Length 48908;
 Best Local Similarity 81.7%; Pred. No. 4.9e-47;
 RESULT 430
 ID AAK66125 standard; DNA; 556 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20937.
 PN WO200517182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 82.3%; Score 202.4; DB 4; Length 556;
 Best Local Similarity 82.6%; Pred. No. 1e-47;
 RESULT 431
 ID AAK66126 standard; DNA; 556 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20938.
 PN WO200517182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 82.3%; Score 202.4; DB 4; Length 556;
 Best Local Similarity 79.9%; Pred. No. 1e-47;
 RESULT 432
 ID AAS36105 standard; DNA; 32195 BP.
 DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1605.
 PN WO200515321-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 82.3%; Score 202.4; DB 4; Length 32195;
 Best Local Similarity 79.9%; Pred. No. 4.8e-47;
 RESULT 433
 ID AAS31538 standard; DNA; 32195 BP.
 DE Human DNA for a novel extracellular matrix protein, Seq ID NO 617.
 PN WO200515368-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 82.3%; Score 202.4; DB 4; Length 32195;
 Best Local Similarity 79.9%; Pred. No. 4.8e-47;
 RESULT 434
 ID AAS31532 standard; DNA; 32195 BP.
 DE Human DNA for a novel extracellular matrix protein, Seq ID NO 611.
 PN WO200515368-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 82.3%; Score 202.4; DB 4; Length 32195;
 Best Local Similarity 79.9%; Pred. No. 4.8e-47;
 RESULT 435
 ID ABK44045 standard; DNA; 32195 BP.
 DE Genomic DNA encoding novel central nervous system protein #260.
 PN WO200515318-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 82.3%; Score 202.4; DB 4; Length 32195;

RESULT 435	
ID AB066856	standard; DNA; 32195 BP.
DB Human polynucleotide SEQ ID NO 611.	
PN US002002336 A1.	
PD 11-APR-2002.	
PA (ROSE/-) ROSEN C A.	
PA (RUBE/-) RUBEN S M.	
PA (BARA/-) BARASH S C.	
PA Query Match Best Local Similarity 22.3%; Score 202.4; DB 6; Length 32195;	
PA Best Local Similarity 79.9%; Pred. No. 4.8e-47;	
RESULT 437	
ID AB066862	standard; DNA; 32195 BP.
DB Human polynucleotide SEQ ID NO 617.	
PN US2002043386-A1.	
PD 11-APR-2002.	
PA (ROSE/-) ROSEN C A.	
PA (RUBE/-) RUBEN S M.	
PA (BARA/-) BARASH S C.	
PA Query Match Best Local Similarity 22.3%; Score 202.4; DB 6; Length 32195;	
PA Best Local Similarity 79.9%; Pred. No. 4.8e-47;	
RESULT 438	
ID ADC1143	standard; DNA; 32195 BP.
DB Human DNA from extracellular matrix gene 112 #1.	
PN US2003059875-A1.	
PD 27-MAR-2003.	
PA (HUMA-) HUMAN GENOME SCI INC.	
PA Query Match Best Local Similarity 22.3%; Score 202.4; DB 10; Length 32195;	
PA Best Local Similarity 79.9%; Pred. No. 4.8e-47;	
RESULT 439	
ID ADC1149	standard; DNA; 32195 BP.
DB Human DNA from extracellular matrix gene 113 #1.	
PN US2003059875-A1.	
PD 27-MAR-2003.	
PA (HUMA-) HUMAN GENOME SCI INC.	
PA Query Match Best Local Similarity 22.3%; Score 202.4; DB 10; Length 32195;	
PA Best Local Similarity 79.9%; Pred. No. 4.8e-47;	
RESULT 440	
ID ADE46799	standard; DNA; 32195 BP.
DB Human cardiovascular system related genomic DNA #365.	
PN WO2003059908-A1.	
PD 27-MAR-2003.	
PA (HUMA-) HUMAN GENOME SCI INC.	
PA Query Match Best Local Similarity 22.3%; Score 202.4; DB 10; Length 32195;	
PA Best Local Similarity 79.9%; Pred. No. 4.8e-47;	
RESULT 441	
ID ADI55030	standard; DNA; 32195 BP.
DB Novel human protein genomic DNA seq id 1233.	
PN US20040183669-A1.	
PD 29-JAN-2004.	
PA (ROSE/-) ROSEN C A.	
PA (RUBE/-) RUBEN S M.	
PA (BARA/-) BARASH S C.	
PA Query Match Best Local Similarity 22.3%; Score 202.4; DB 12; Length 32195;	
PA Best Local Similarity 79.9%; Pred. No. 4.8e-47;	
RESULT 442	
ID ADJ0217	standard; DNA; 32195 BP.
DB Human cardiovascular system associated polypeptide-related DNA SeqID1605.	
PN US2004005575-A1.	
PD 08-JAN-2004.	
PA (HUMA-) HUMAN GENOME SCI INC.	
PA Query Match Best Local Similarity 22.3%; Score 202.4; DB 13; Length 32195;	
PA Best Local Similarity 79.9%; Pred. No. 4.8e-47;	
RESULT 443	
ID ACN7205	standard; DNA; 34079 BP.
DB Human periodontal disease related gene COL18A1 SEQ ID NO:115.	
PN WO200517182-A2.	
PD 09-AUG-2001.	
PA (HUMA-) HUMAN GENOME SCI INC.	
PA Query Match Best Local Similarity 22.3%; Score 202.4; DB 13; Length 34079;	
PA Best Local Similarity 81.2%; Pred. No. 4.9e-47;	
RESULT 444	
ID AAKB3781	standard; DNA; 37664 BP.
DB Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38593.	
PN WO200517182-A2.	
PD 09-AUG-2001.	
PA (HUMA-) HUMAN GENOME SCI INC.	
PA Query Match Best Local Similarity 22.3%; Score 202.4; DB 4; Length 37664;	
PA Best Local Similarity 81.2%; Pred. No. 5e-47;	
RESULT 445	
ID ABQ18157	standard; DNA; 43712 BP.
DB Human soft tissue sarcoma-upregulated DNA - SEQ ID 1576.	
PN WO200404938-A2.	
PD 10-JUN-2004.	
PA (PROT-) PROTEIN DESIGN LABS INC.	
PA Query Match Best Local Similarity 22.3%; Score 202.4; DB 12; Length 43712;	
PA Best Local Similarity 77.6%; Pred. No. 5.3e-47;	
RESULT 446	
ID AAK8782	standard; DNA; 61710 BP.
DB Human immune/hematopoietic antigen genomic sequence SEQ ID NO:38594.	
PN WO200517182-A2.	
PD 09-AUG-2001.	
PA (HUMA-) HUMAN GENOME SCI INC.	
PA Query Match Best Local Similarity 22.3%; Score 202.4; DB 4; Length 61710;	
PA Best Local Similarity 81.2%; Pred. No. 6.1e-47;	
RESULT 447	
ID AAL57580	standard; cDNA; 93273 BP.
DB Human GTPase activating protein-like cDNA.	
PN WO2003059148-A2.	
PD 24-JUL-2003.	
PA (GENE-) GENIE LOGIC INC.	
PA (LGBI-) LG BIOMEDICAL INST.	
PA Query Match Best Local Similarity 22.3%; Score 202.4; DB 9; Length 93273;	
PA Best Local Similarity 79.9%; Pred. No. 7.2e-47;	
RESULT 448	
ID ABD32827	standard; DNA; 129381 BP.
DB Human cancer-associated genomic DNA HD17-008.	
PN WO2004074320-A2.	
PD 02-SEP-2004.	
PA (SAGR-) SAGRES DISCOVERY INC.	
PA Query Match Best Local Similarity 22.3%; Score 202.4; DB 13; Length 129381;	
PA Best Local Similarity 81.2%; Pred. No. 8.1e-47;	
RESULT 449	
ID AZ50359	standard; DNA; 9365 BP.
DB Human CD39-L4 genomic DNA.	
PN WO20000441-A2.	
PD 27-JAN-2000.	
PA (HYSE-) HYSEQ INC.	
PA Query Match Best Local Similarity 22.3%; Score 202.4; DB 3; Length 9365;	
PA Best Local Similarity 78.6%; Pred. No. 3.4e-47;	
RESULT 450	
ID AAF63405	standard; DNA; 9365 BP.
DB Human CD39 like Protein CD39-L4 partial DNA sequence.	
PN WO200110205-A1.	
PD 15-FEB-2001.	
PA (HYSE-) HYSEQ INC.	
PA Query Match Best Local Similarity 22.3%; Score 202.2; DB 4; Length 9365;	
PA Best Local Similarity 78.6%; Pred. No. 3.4e-47;	
RESULT 451	
ID AAF63405	standard; DNA; 14747 BP.
DB Human CD39 like Protein CD39-L4 genomic DNA sequence.	
PN WO200110205-A1.	
PD 15-FEB-2001.	
PA (HYSE-) HYSEQ INC.	
PA Query Match Best Local Similarity 22.3%; Score 202.2; DB 4; Length 14747;	
PA Best Local Similarity 78.6%; Pred. No. 4e-47;	
RESULT 452	
ID AAF63407	standard; DNA; 15977 BP.
DB Human CD39 like protein CD39-L4 genomic DNA sequence #2.	
PN WO200110205-A1.	
PD 15-FEB-2001.	
PA (HYSE-) HYSEQ INC.	
PA Query Match Best Local Similarity 22.3%; Score 202.2; DB 4; Length 15977;	
PA Best Local Similarity 78.6%; Pred. No. 4.1e-47;	
RESULT 453	
ID ACM44382	standard; DNA; 30558 BP.
DB Human genomic sequence hCG15773.	
PN WO200303826-A2.	
PD 12-SEP-2003.	
PA (SAGR-) SAGRES DISCOVERY.	

Query Match 22.3%; Score 202.2; DB 11; Length 30558;
 Best Local Similarity 85.8%; Pred. No. 5.3e-47;
 RESULT 454
 ID ABN96331 standard; DNA; 99014 BP.
 DE Gene #3429 used to diagnose liver cancer.
 PN WO2002229103-A2.
 PD 11-APR-2002.

PA (GENE-) GENE LOGIC INC.
 Query Match 22.3%; Score 202.2; DB 6; Length 99014;
 Best Local Similarity 79.5%; Pred. No. 8.4e-47;
 RESULT 455
 ID ACM1994 standard; DNA; 109586 BP.
 DE Human genomic Sequence hCG23847.
 PN WO2003073856-A2.
 PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.3%; Score 202.2; DB 11; Length 109586;
 Best Local Similarity 83.2%; Pred. No. 8.7e-47;
 RESULT 456
 ID ADP03055 standard; cDNA; 124987 BP.
 DE Human housekeeping gene cDNA #96.
 PN JF2004135552-A.
 PD 13-MAY-2004.

PA (NTIGA-) NGK INSULATORS LTD.
 Query Match 22.3%; Score 202.2; DB 12; Length 124987;
 Best Local Similarity 82.1%; Pred. No. 9.1e-47;
 RESULT 457
 ID ADPS8553 standard; cDNA; 124990 BP.
 DE Human housekeeping gene cDNA .Sequence SEQ ID NO:96.
 PN WO2004035785-A1.
 PD 29-APR-2004.

PA (NIGA-) NGK INSULATORS LTD.
 Query Match 22.3%; Score 202.2; DB 13; Length 124990;
 Best Local Similarity 82.1%; Pred. No. 9.1e-47;
 RESULT 458
 ID ACH23975 standard; cDNA; 502 BP.
 DE Human adult ovary cDNA #4355.
 PN US2003073653-A1.
 PD 17-APR-2003.

PA (DRMA-) DRMANAC R T.
 PA (LABA-) LABAT I.
 PA (STAC-) STACHE-CRAIN B.
 PA (DICK-) DICKSON M C.
 PA (JONE-) JONES L W.
 Query Match 22.3%; Score 202; DB 9; Length 502;
 Best Local Similarity 72.7%; Pred. No. 1.2e-47;
 RESULT 459
 ID ADD19251 standard; cDNA; 843 BP.
 DE Human cDNA from secreted protein gene 68.
 PN WO2003052377-A2.
 PD 26-JUN-2003.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.3%; Score 202; DB 10; Length 843;
 Best Local Similarity 81.5%; Pred. No. 1.5e-47;
 RESULT 460
 ID ADD1217 standard; cDNA; 878 BP.
 DE Human cDNA from secreted protein gene 34.
 PN WO2003052377-A2.
 PD 26-JUN-2003.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.3%; Score 202; DB 10; Length 878;
 Best Local Similarity 81.5%; Pred. No. 1.5e-47;
 RESULT 461
 ID ADDM02980 standard; cDNA; 1960 BP.
 DE Human cDNA of the invention SEQ ID NO:1665.
 PN EP1347046-A1.
 PD 24-SEP-2003.

PA (REAS-) RIS ASSOC BIOTECHNOLOGY.
 Query Match 22.3%; Score 202; DB 11; Length 1960;
 Best Local Similarity 78.2%; Pred. No. 2.1e-47;
 RESULT 462
 ID ADD18777 standard; DNA; 8672 BP.
 DE Human disease related protein DNA sequence SeqID208.
 PN WO2003004622-A2.

PN WO2003018621-A2.
 PD 06-MAR-2003.
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 Query Match 22.3%; Score 202; DB 10; Length 8672;
 Best Local Similarity 74.6%; Pred. No. 3.7e-47;
 RESULT 463
 ID ARK7319 standard; DNA; 15090 BP.
 DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:27131.
 PN WO200157192-A2.
 PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.3%; Score 202; DB 4; Length 15090;
 Best Local Similarity 83.0%; Pred. No. 4.6e-47;
 RESULT 464
 ID ABK69842 standard; DNA; 15090 BP.
 DE Human Secreted protein gene 22 genomic DNA fragment #3.
 PN WO200226931-A2.
 PD 04-APR-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.3%; Score 202; DB 6; Length 15090;
 Best Local Similarity 83.0%; Pred. No. 4.6e-47;
 RESULT 465
 ID ABK69843 standard; DNA; 15090 BP.
 DE Human secreted protein gene 22 genomic DNA fragment #4.
 PN WO200226931-A2.
 PD 04-APR-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.3%; Score 202; DB 6; Length 15090;
 Best Local Similarity 83.0%; Pred. No. 4.6e-47;
 RESULT 466
 ID ACC50857 standard; cDNA; 15090 BP.
 DE Human secreted protein BAC clone SEQ ID NO 1037.
 PN WO200295010-A2.
 PD 28-NOV-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.3%; Score 202; DB 8; Length 15090;
 Best Local Similarity 83.0%; Pred. No. 4.6e-47;
 RESULT 467
 ID ACC50858 standard; cDNA; 15090 BP.
 DE Human secreted protein BAC clone SEQ ID NO 1038.
 PN WO200295010-A2.
 PD 28-NOV-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.3%; Score 202; DB 8; Length 15090;
 Best Local Similarity 83.0%; Pred. No. 4.6e-47;
 RESULT 468
 ID ABZ71480 standard; DNA; 15090 BP.
 DE Secreted protein gene 12 genomic Fragment HAUAI83, SEQ ID NO:590.
 PN WO200276488-A1.
 PD 03-OCT-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.3%; Score 202; DB 8; Length 15090;
 Best Local Similarity 83.0%; Pred. No. 4.6e-47;
 RESULT 469
 ID ABZ71479 standard; DNA; 15090 BP.
 DE Secreted Protein gene 12 genomic fragment HAUAI83, SEQ ID NO:589.
 PN WO200276488-A1.
 PD 03-OCT-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.3%; Score 202; DB 8; Length 15090;
 Best Local Similarity 83.0%; Pred. No. 4.6e-47;
 RESULT 470
 ID ADB91835 standard; DNA; 15090 BP.
 DE Human secreted protein related DNA #SEQ ID 781.
 PN WO2003004622-A2.
 PD 16-JAN-2003.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.3%; Score 202; DB 9; Length 15090;
 Best Local Similarity 83.0%; Pred. No. 4.6e-47;
 RESULT 471
 ID ADB91836 standard; DNA; 15090 BP.
 DE Human secreted protein related DNA #SEQ ID 782.
 PN WO2003004622-A2.

PD 16-JAN-2003. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.3%; Score 202; DB 9; Length 15090; Best Local Similarity 83.0%; Pred. No. 4.6e-47; RESULT 472. ID ADC74610 standard; DNA; 15090 BP. DE Human secreted protein-related DNA - SEQ ID 1243. PN WO2003038063-A2.

PD 08-MAY-2003. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.3%; Score 202; DB 10; Length 15090; Best Local Similarity 83.0%; Pred. No. 4.6e-47; RESULT 473. ID ADC74611 standard; DNA; 15090 BP. DE Human secreted protein-related DNA - SEQ ID 1244. PN WO2003038063-A2.

PD 08-MAY-2003. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.3%; Score 202; DB 10; Length 15090; Best Local Similarity 83.0%; Pred. No. 4.6e-47; RESULT 474. ID ADD8131 standard; cDNA; 15090 BP. DE cDNA clone in ARCC deposit #25. PN WO2003038063-A2.

PD 14-NOV-2002. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.3%; Score 202; DB 10; Length 15090; Best Local Similarity 83.0%; Pred. No. 4.6e-47; RESULT 475. ID ADD8130 standard; cDNA; 15090 BP. DE cDNA clone in ARCC deposit #24. PN WO2003038063-A2.

PD 14-NOV-2002. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.3%; Score 202; DB 10; Length 15090; Best Local Similarity 83.0%; Pred. No. 4.6e-47; RESULT 476. ID ADD8124 standard; DNA; 15090 BP. DE BAC fragment containing human secreted protein gene #302. PN WO2003038063-A2.

PD 27-DEC-2002. PA (HOMA-) HUMAN GENOME SCI INC. Query Match 22.3%; Score 202; DB 10; Length 15090; Best Local Similarity 83.0%; Pred. No. 4.6e-47; RESULT 477. ID ADD5725 standard; DNA; 15090 BP. DE BAC fragment containing human secreted protein gene #302. PN WO2003038063-A2.

PD 27-DEC-2002. PA (HOMA-) HUMAN GENOME SCI INC. Query Match 22.3%; Score 202; DB 10; Length 15090; Best Local Similarity 83.0%; Pred. No. 4.6e-47; RESULT 478. ID ADD0230 standard; DNA; 32433 BP. DE Human FLT3 carcinoma associated gene, SEQ ID NO:1148. PN WO2003057146-A2.

PD 17-JUL-2003. PA (SAGR-) SAGRES DISCOVERY. Query Match 22.3%; Score 202; DB 9; Length 32433; Best Local Similarity 80.3%; Pred. No. 6.2e-47; RESULT 479. ID ADB72368 standard; DNA; 32433 BP. DE Human FLT3 gene. PN WO2003058583-A2.

PD 30-JAN-2003. PA (SAGR-) SAGRES DISCOVERY. Query Match 22.3%; Score 202; DB 10; Length 32433; Best Local Similarity 80.3%; Pred. No. 6.2e-47; RESULT 480. ID ADB95878 standard; DNA; 32433 BP. DE Human FLT3 gene genomic DNA sequence. PN WO2003039484-A2.

PD 15-MAY-2003. PA (SAGR-) SAGRES DISCOVERY. Query Match 22.3%; Score 202; DB 10; Length 32433; Best Local Similarity 80.3%; Pred. No. 6.2e-47; RESULT 481. ID ABD33115 standard; DNA; 69652 BP. DE Human cancer-associated (CA) gene HD07-011. PN WO20040058146-A2.

PD 15-JUL-2004. PA (SAGR-) SAGRES DISCOVERY INC. Query Match 22.3%; Score 202; DB 13; Length 69652; Best Local Similarity 77.1%; Pred. No. 8.3e-47; RESULT 482. ID ABD33868 standard; DNA; 238417 BP. DE Human cancer-associated genomic DNA HD17-053. PN WO2004074320-A2.

PD 02-SEP-2004. PA (SAGR-) SAGRES DISCOVERY INC. Query Match 22.3%; Score 202; DB 13; Length 238417; Best Local Similarity 82.8%; Pred. No. 1.3e-46; RESULT 483. ID AAK79410 standard; DNA; 4883 BP. DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:34222. PN WO200517182-A2.

PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.2%; Score 201.8; DB 4; Length 4883; Best Local Similarity 78.1%; Pred. No. 3.4e-47; RESULT 484. ID AD06434 standard; cDNA; 8331 BP. DE Novel human cDNA sequence #1595. PN EPI1440981-A2.

PD 28-JUN-2004. PA (REAS-) RES ASSOC BIOTECHNOLOGY. Query Match 22.2%; Score 201.8; DB 12; Length 8331; Best Local Similarity 83.5%; Pred. No. 4.2e-47; RESULT 485. ID AAS33461 standard; DNA; 9192 BP. DE DNA encoding human secreted protein, Seq ID No 744. PN WO200515326-A2.

PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.2%; Score 201.8; DB 4; Length 9192; Best Local Similarity 81.0%; Pred. No. 4.4e-47; RESULT 486. ID AAL33467 standard; DNA; 11991 BP. DE Human musculoskeletal system related polynucleotide SEQ ID NO 2942. PN WO200515367-A1.

PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.2%; Score 201.8; DB 4; Length 11991; Best Local Similarity 76.9%; Pred. No. 4.8e-47; RESULT 487. ID AAL07205 standard; DNA; 11991 BP. DE Human reproductive system related antigen DNA SEQ ID NO: 9893. PN WO200515320-A2.

PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.2%; Score 201.8; DB 4; Length 11991; Best Local Similarity 76.9%; Pred. No. 4.8e-47; RESULT 488. ID ABX59565 standard; cDNA; 11991 BP. DE cDNA encoding novel human musculoskeletal system antigen #1909. PN US2002147140-A1.

PD 10-OCT-2002. PA (ROSE/) ROSEN C. A. Query Match 22.2%; Score 201.8; DB 4; Length 11991; Best Local Similarity 76.9%; Pred. No. 4.8e-47; RESULT 489. ID ADJ30315 standard; DNA; 11991 BP. DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2942. PN US2004009488-A1.

PD 15-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.8; DB 12; Length 11991;
 Best Local Similarity 76.9%; Pred. No. 4.8e-47;
 RESULT 490
 ID AAS3462 standard; DNA; 25715 BP.
 DE DNA encoding human secreted protein, Seq ID No 745.
 PN WO200155326-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.8; DB 4; Length 25715;
 Best Local Similarity 81.0%; Pred. No. 6.5e-17;
 RESULT 491
 ID ACN44690 standard; DNA; 47243 BP.
 DE Human genomic sequence hgc16501.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.2%; Score 201.8; DB 11; Length 47243;
 Best Local Similarity 82.3%; Pred. No. 8.2e-47;
 RESULT 492
 ID ADM97422 standard; DNA; 76341 BP.
 DE Prostate and breast cancer associated human gene SRD5A2.
 PN WO2004028346-A2.
 PD 08-APR-2004.
 PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 Query Match 22.2%; Score 201.8; DB 12; Length 76341;
 Best Local Similarity 83.5%; Pred. No. 9.9e-47;
 RESULT 493
 ID ADQ9518 standard; DNA; 100762 BP.
 DE Human cancer-associated (CA) gene, sequence SEQ ID NO:154.
 PN WO2004058288-A1.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.2%; Score 201.8; DB 12; Length 100762;
 Best Local Similarity 78.8%; Pred. No. 1.1e-46;
 RESULT 494
 Query Match 22.2%; Score 201.8; DB 10; Length 110000;
 Best Local Similarity 78.6%; Pred. No. 1.1e-46;
 RESULT 495
 ID AAD02697 standard; DNA; 160552 BP.
 DE Human glycosyl sulfotransferase-4 (GST-4) genomic DNA.
 PN WO200106015-A1.
 PD 25-JAN-2001.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 22.2%; Score 201.8; DB 4; Length 160552;
 Best Local Similarity 81.0%; Pred. No. 1.3e-46;
 RESULT 496
 ID ABD3232 standard; DNA; 161531 BP.
 DE Human cancer-associated (CA) gene HD07-038.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.2%; Score 201.8; DB 13; Length 161531;
 Best Local Similarity 81.0%; Pred. No. 1.3e-46;
 RESULT 497
 ID ADL13775 standard; DNA; 173805 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #307.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 22.2%; Score 201.8; DB 10; Length 173805;
 Best Local Similarity 83.5%; Pred. No. 1.4e-46;
 RESULT 498
 ID ACN44626 standard; DNA; 175077 BP.
 DE Human genomic sequence hgc1974.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.2%; Score 201.8; DB 11; Length 175077;
 Best Local Similarity 79.9%; Pred. No. 1.4e-46;
 RESULT 499
 ID ADB43315 standard; DNA; 202100 BP.

DE Human IDE/ KNSL1 genomic sequence, SEQ ID 484.
 PN WO2003054143-A2.
 PD 03-JUL-2003.
 PA (NEUR-) NEUROGENETICS INC.
 Best Local Similarity 81.2%; Pred. No. 1.4e-46;
 RESULT 500
 ID ADH54357 standard; DNA; 202100 BP.
 DE Human IDE/KNSL1 gene DNA sequence SeqID484.
 PN US2003224380-A1.
 PD 04-DEC-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 Query Match 22.2%; Score 201.8; DB 12; Length 202100;
 Best Local Similarity 81.2%; Pred. No. 1.4e-46;
 RESULT 501
 ID ADP7118 standard; DNA; 276820 BP.
 DE Human Adams2 gene.
 PN WO2003031594-A2.
 PD 17-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 22.2%; Score 201.8; DB 11; Length 276820;
 Best Local Similarity 83.7%; Pred. No. 1.6e-46;
 RESULT 502
 ID AAS32713 standard; DNA; 2666 BP.
 DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 667.
 PN WO200155319-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.6; DB 4; Length 2666;
 Best Local Similarity 77.7%; Pred. No. 3.1e-47;
 RESULT 503
 ID ADP06622 standard; cDNA; 3677 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 128.
 PN EP1447413-A2.
 PD 18-AUG-2004.
 PA (REAS-) RBS ASSOC BIOTECHNOLOGY.
 Query Match 22.2%; Score 201.6; DB 13; Length 3677;
 Best Local Similarity 83.0%; Pred. No. 3.5e-47;
 RESULT 504
 ID AAK91537 standard; DNA; 8896 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO 5113.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.6; DB 4; Length 8896;
 Best Local Similarity 77.7%; Pred. No. 4.9e-47;
 RESULT 505
 ID AAU57794 standard; DNA; 8896 BP.
 DE Human colorectal cancer antigen coding sequence SEQ ID NO 331.
 PN WO200155350-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.6; DB 4; Length 8896;
 Best Local Similarity 77.7%; Pred. No. 4.9e-47;
 RESULT 506
 ID AAS37112 standard; DNA; 8896 BP.
 DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 666.
 PN WO200155319-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.6; DB 4; Length 8896;
 Best Local Similarity 77.7%; Pred. No. 4.9e-47;
 RESULT 507
 ID ABS9971 standard; DNA; 8896 BP.
 DE Genomic DNA #175 encoding human colorectal cancer related protein.
 PN US2002115919-A1.
 PD 29-AUG-2002.
 PA (ROSE-) ROSEN C A.
 PA (RUBB-) RUBEN S M.
 PA (BARA-) BARASH S C.
 Query Match 22.2%; Score 201.6; DB 6; Length 8896;
 Best Local Similarity 77.7%; Pred. No. 4.9e-47;

RESULT 508
ID ADB93124 standard; DNA; 8996 BP.
DE Human colorectal cancer related polypeptide DNA #175.
PN US200305420-A1.
PD 20-MAR-2003.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 10; Length 8896;
Best Local Similarity 77.7%; Pred. No. 4.9e-47;

RESULT 509
ID AAL60675 standard; DNA; 12430 BP.
DE Human ataxia telangiectasia and Rad-3-related (ATR) clone8 gene.
PN WO2003042214-A2.

PA (BAYU-) BAYLOR COLLEGE MEDICINE.
Query Match 22.2%; Score 201.6; DB 9; Length 12430;
Best Local Similarity 85.5%; Pred. No. 5.6e-47;

RESULT 510
ID AAL6076 standard; DNA; 1405 BP.
DE PDC353 knockout construct DNA.
PN WO2003042214-A2.

PA (BAYU-) BAYLOR COLLEGE MEDICINE.
Query Match 22.2%; Score 201.6; DB 9; Length 14405;
Best Local Similarity 85.5%; Pred. No. 5.9e-47;

RESULT 511
ID AAK84138 standard; DNA; 17758 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38950.
PN WO201517182-A2.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 17758;
Best Local Similarity 83.0%; Pred. No. 6.4e-47;

RESULT 512
ID AA199172 standard; DNA; 32134 BP.
DE Human excretory related polynucleotide SEQ ID NO 936.
PN WO200155313-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 32134;
Best Local Similarity 77.7%; Pred. No. 8.1e-47;

RESULT 513
ID AA163522 standard; DNA; 32134 BP.
DE Human kidney related polynucleotide SEQ ID NO 837.
PN WO200155320-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 5; Length 32134;
Best Local Similarity 77.7%; Pred. No. 8.1e-47;

RESULT 514
ID AA199173 standard; DNA; 32192 BP.
DE Human excretory related polynucleotide SEQ ID NO 937.
PN WO200155313-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 32192;
Best Local Similarity 77.7%; Pred. No. 8.1e-47;

RESULT 515
ID AAI63523 standard; DNA; 32192 BP.
DE Human kidney related polynucleotide SEQ ID NO 838.
PN WO200155320-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 5; Length 32192;
Best Local Similarity 77.7%; Pred. No. 8.1e-47;

RESULT 516
ID AAI69767 standard; DNA; 35100 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24579.
PN WO2001517182-A2.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 35100;
Best Local Similarity 77.7%; Pred. No. 8.3e-47;

RESULT 517
ID AAK65700 standard; DNA; 35100 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20512.
PN WO2001517182-A2.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 35100;
Best Local Similarity 77.7%; Pred. No. 8.3e-47;

RESULT 518
ID AAK69166 standard; DNA; 35115 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24578.
PN WO2001517182-A2.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 35115;
Best Local Similarity 77.7%; Pred. No. 8.3e-47;

RESULT 519
ID AAK65699 standard; DNA; 35115 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20511.
PN WO2001517182-A2.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 35115;
Best Local Similarity 77.7%; Pred. No. 8.3e-47;

RESULT 520
ID ACN44146 standard; DNA; 50602 BP.
DE Human genomic sequence hgG28572.
PN WO2003073826-A2.

PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.2%; Score 201.6; DB 4; Length 35115;
Best Local Similarity 77.7%; Pred. No. 8.3e-47;

RESULT 521
ID AAK90201 standard; DNA; 119950 BP.
DE Human Yes1 gene.
PN WO99352290-A1.

PD 15-JUL-1999.

PA (MILL-) MILLENNIUM PHARM INC.
Query Match 22.2%; Score 201.6; DB 2; Length 119950;
Best Local Similarity 81.7%; Pred. No. 1.3e-46;

RESULT 522
ID ADP65433 standard; DNA; 154068 BP.
DE Human sequence from clone RPI-1-36312 on chromosome 1, complete DNA.
PN WO2003072827-A1.

PD 04-SEP-2003.

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 22.2%; Score 201.6; DB 11; Length 154068;
Best Local Similarity 81.2%; Pred. No. 1.5e-46;

RESULT 523
ID ACH21579 standard; cDNA; 406 BP.
DE Human adult liver cDNA #1191.
PN US2003073623-A1.

PD 17-APR-2003.

PA (DRMA-) DRMANAC R T.
PA (LBBM-) LABBT I.
PA (STAC-) STACHE-CHAIN B.
PA (DICK-) DICKSON M C.
PA (JONE-) JONES L W.

Query Match 22.2%; Score 201.4; DB 9; Length 406;
Best Local Similarity 82.4%; Pred. No. 1.7e-47;

RESULT 524
ID AAH18654 standard; cDNA; 6020 BP.
DE Human cDNA sequence SEQ ID NO:18887.
PN EP1074617-A2.

PD 07-FEB-2001.

PA (HLBL-) HELIX RES INST.
Query Match 22.2%; Score 201.4; DB 4; Length 6020;
Best Local Similarity 72.9%; Pred. No. 4.8e-47;

RESULT 525
ID AAV3455 standard; DNA; 11722 BP.
DE Human MHC class I chain-related gene A (MICA).
PN WO9819167-A2.

PD 07-MAY-1998.

PA (HUTC-) HUTCHINSON CANCER RES CENT FRBD.

Query Match 22.2%; Score 201.4; DB 2; Length 11722;
 Best Local Similarity 83.6%; Pred. No. 6.2e-47;
 RESULT 526
 ID ADE6443 standard; cDNA; 11722 BP.
 DE Human MICA cDNA SEQ ID NO:1.
 PN WO2003089516-A2.
 PD 30-OCT-2003.

PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 Best Local Similarity 22.2%; Score 201.4; DB 10; Length 11722;
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3735.
 PN WO200155314-A2.
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.4; DB 4; Length 15783;
 Best Local Similarity 81.2%; Pred. No. 7e-47;
 RESULT 528
 ID AAS39803 standard; DNA; 15783 BP.
 DE Genomic sequence #222 encoding human colon associated polypeptide.
 PN WO200155305-A2.
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.4; DB 5; Length 15783;
 Best Local Similarity 81.2%; Pred. No. 7e-47;
 RESULT 529
 ID ADB32763 standard; DNA; 15783 BP.
 DE Human novel colon related polypeptide DNA SEQ ID NO 700.
 PN US2003050231-A1.
 PD 13-MAR-2003.

PA (ROSE-) ROSEN C A.
 PA (RUBE-) RUBEN S M.
 PA (BARA-) BARBASH S C.
 Query Match 22.2%; Score 201.4; DB 9; Length 15783;
 Best Local Similarity 81.2%; Pred. No. 7e-47;
 RESULT 530
 ID ABAL4191 standard; DNA; 16159 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 10822.
 PN WO201159053-A2.
 PD 16-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.4; DB 5; Length 16159;
 Best Local Similarity 85.0%; Pred. No. 7.1e-47;
 RESULT 531
 ID ACM44470 standard; DNA; 42954 BP.
 DE Human genomic sequence hCG40844.
 PN WO2003073026-A2.
 PD 12-SEP-2003.

PA (SAGR-) SACRES DISCOVERY.
 Query Match 22.2%; Score 201.4; DB 11; Length 42954;
 Best Local Similarity 81.2%; Pred. No. 1e-46;
 RESULT 532
 ID ADC60735 standard; DNA; 50000 BP.
 DE Human slingshot-related DNA 9.
 PN JP2003102483-A.
 PD 08-APR-2003.

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 Query Match 22.2%; Score 201.4; DB 10; Length 50000;
 Best Local Similarity 82.4%; Pred. No. 1.1e-6;
 RESULT 533
 ID ACN44290 standard; DNA; 59856 BP.
 DE Human genomic sequence hCG24994.
 PN WO2003073026-A2.
 PD 12-SEP-2003.

PA (SAGR-) SACRES DISCOVERY.
 Query Match 22.2%; Score 201.4; DB 11; Length 59856;
 Best Local Similarity 81.2%; Pred. No. 1.2e-46;
 RESULT 534
 ID AAD50739 standard; DNA; 64467 BP.
 DE Human kinase gene.
 PN WO200157182-A2.

Query Match 22.2%; Score 201.4; DB 8; Length 64467;
 Best Local Similarity 74.6%; Pred. No. 1.2e-46;

RESULT 535
 ID ACH0010 standard; DNA; 64467 BP.
 DE Human kinase protein genomic DNA.
 Query Match 22.2%; Score 201.4; DB 9; Length 64467;
 Best Local Similarity 74.6%; Pred. No. 1.2e-46;
 RESULT 535
 ID ADD15783 standard; DNA; 64467 BP.
 DE Human MEK kinase subfamily kinase genomic DNA.
 PN US652946-B1.
 PD 24-JUN-2003.

PA (APPL-) APPLERA CORP.
 Query Match 22.2%; Score 201.4; DB 10; Length 64467;
 Best Local Similarity 74.6%; Pred. No. 1.2e-46;
 RESULT 537
 ID ABL64403 standard; DNA; 167343 BP.
 DE Stomach cancer related gene sequence SEQ ID NO:2740.
 PN WO2001594629-A2.
 PD 13-DEC-2001.

PA (AVAL-) AVALON PHARM.
 Query Match 22.2%; Score 201.4; DB 6; Length 167343;
 Best Local Similarity 76.1%; Pred. No. 1.7e-46;
 RESULT 538
 ID ABL67239 standard; DNA; 167343 BP.
 DE -Thyroid cancer related gene sequence SEQ ID NO:5746.
 PN WO2001594629-A2.
 PD 13-DEC-2001.

PA (AVAL-) AVALON PHARM.
 Query Match 22.2%; Score 201.4; DB 6; Length 167343;
 Best Local Similarity 76.1%; Pred. No. 1.7e-46;
 RESULT 539
 ID ABD32715 standard; DNA; 337344 BP.
 DE Human cancer-associated genomic DNA HD14-044.
 PN WO2004074320-A2.
 PD 02-SEP-2004.

PA (SAGR-) SACRES DISCOVERY INC.
 Query Match 22.2%; Score 201.4; DB 13; Length 337344;
 Best Local Similarity 81.2%; Pred. No. 2.3e-46;
 RESULT 540
 ID AAH14294 standard; cDNA; 1557 BP.
 DE Human cDNA sequence SEQ ID NO:11638.
 PN EP1074617-A2.
 PD 07-FEB-2001.

PA (HELI-) HELIX RES INST.
 Query Match 22.2%; Score 201.2; DB 4; Length 1557;
 Best Local Similarity 85.8%; Pred. No. 3.3e-47;

RESULT 541
 ID ADQ19190 standard; DNA; 1557 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2009.
 PN WO2004048938-A2.
 PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 22.2%; Score 201.2; DB 12; Length 1557;
 Best Local Similarity 85.8%; Pred. No. 3.3e-47;

RESULT 542
 ID AAK87586 standard; DNA; 14426 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42398.
 PN WO20051712-A2.
 PD 09-AUG-2005.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.2; DB 4; Length 14426;
 Best Local Similarity 82.1%; Pred. No. 7.7e-47;

RESULT 543
 ID AAK71817 standard; DNA; 14426 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26629.
 PN WO20051712-A2.
 PD 09-AUG-2005.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.2; DB 4; Length 14426;
 Best Local Similarity 82.1%; Pred. No. 7.7e-47;

RESULT 544
 ID AAK73115 standard; DNA; 14426 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27927.
 PN WO200517182-A2.

PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.2; DB 4; Length 14426;
 Best Local Similarity 82.1%; Pred. No. 7.7e-47;
 RESULT 545
 ID AAI62924 standard; DNA; 1426 BP.
 DB Human genomic DNA SEQ ID NO 252.
 PN WO200155419-A1.

PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.2; DB 4; Length 14426;
 Best Local Similarity 82.1%; Pred. No. 7.7e-47;
 RESULT 546
 ID ABZ71676 standard; DNA; 1426 BP.
 DE Secreted protein gene 391 genomic fragment HEBFC45, SEQ ID NO:1823.
 PN WO200277013-A2.

PD 03-OCT-2002. PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.2; DB 8; Length 14426;
 Best Local Similarity 82.1%; Pred. No. 7.7e-47;
 RESULT 547
 ID ABZ68198 standard; DNA; 1426 BP.
 DE Human secreted protein encoding genomic DNA SEQ ID NO 1721.
 PN WO200277186-A2.

PD 03-OCT-2002. PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.2; DB 10; Length 14426;
 Best Local Similarity 82.1%; Pred. No. 7.7e-47;
 RESULT 548
 ID ABA13324 standard; DNA; 27733 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 11655.
 PN WO200159063-A2.

PD 16-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.2; DB 5; Length 27733;
 Best Local Similarity 79.6%; Pred. No. 9.9e-47;
 RESULT 549
 ID AAK66517 standard; DNA; 21869 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21329.
 PN WO200157182-A2.

PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.2; DB 4; Length 27869;
 Best Local Similarity 76.6%; Pred. No. 9.9e-47;
 RESULT 550
 ID ABA19635 standard; DNA; 27869 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 11966.
 PN WO200159063-A2.

PD 16-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.2; DB 5; Length 27869;
 Best Local Similarity 76.6%; Pred. No. 9.9e-47;
 RESULT 551
 ID ADQ97164 standard; DNA; 145985 BP.
 DE Human cancer associated sequence HDI-08-009, SEQ ID 140.
 PN WO2004060301-A2.

PD 22-JUL-2004. PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.2%; Score 201.2; DB 12; Length 145985;
 Best Local Similarity 83.1%; Pred. No. 1.9e-46;
 RESULT 552
 ID ABB33272 standard; DNA; 227246 BP.
 DE Human cancer-associated (CA) gene HD07-047.
 PN WO2004058146-A2.

PA (SAGR-) SAGRES DISCOVERY INC. Query Match 22.2%; Score 201.2; DB 13; Length 227246;
 Best Local Similarity 80.7%; Pred. No. 2.2e-46;
 RESULT 553
 ID AAK51619 standard; DNA; 370 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19981.
 PN WO20017182-A2.

PA (SAGR-) SAGRES DISCOVERY INC. Query Match 22.2%; Score 201; DB 13; Length 39699;

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.2%; Score 201; DB 4; Length 370;
 Best Local Similarity 81.4%; Pred. No. 2.2e-47;
 RESULT 554
 ID ABV4137 standard; cDNA; 477 BP.
 DB Human prostate expression marker cDNA 46128.
 PN WO200160890-A2.

PD 23-AUG-2001. PA (MILL-) MILLENIUM PREDICTIVE MEDICINE INC.
 Query Match 22.2%; Score 201; DB 5; Length 477;
 Best Local Similarity 81.4%; Pred. No. 2.4e-47;
 RESULT 555
 ID ABQ71599 standard; cDNA; 2616 BP.
 DE Human Mmp7 encoding cDNA SEQ ID NO 151.
 PN WO200240715-A2.

PD 23-MAY-2002. PA (INCY-) INCYTE GENOMICS INC.
 Query Match 22.2%; Score 201; DB 6; Length 2616;
 Best Local Similarity 81.4%; Pred. No. 4.6e-47;
 RESULT 556
 ID ABD33088 standard; cDNA; 3404 BP.
 DE Human cancer-associated (CA) cDNA HR07-004.
 PN WO2004058146-A2.

PD 15-JUL-2004. PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.2%; Score 201; DB 13; Length 3404;
 Best Local Similarity 81.4%; Pred. No. 5.1e-47;
 RESULT 557
 ID ADJ96554 standard; DNA; 3463 BP.
 DE Human calcium/calmodulin-dependent protein kinase Nuak2 DNA SeqID 11.
 PN WO2004066838-A2.

PD 22-JAN-2004. PA (SUGE-) SUGEN INC.
 Query Match 22.2%; Score 201; DB 12; Length 3463;
 Best Local Similarity 81.4%; Pred. No. 5.1e-47;
 RESULT 558
 ID AAK74096 standard; DNA; 21777 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28908.
 PN WO200157182-A2.

PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201; DB 12; Length 3463;
 Best Local Similarity 83.9%; Pred. No. 1e-46;
 RESULT 559
 ID ABR15339 standard; DNA; 24292 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 8270.
 PN WO200159063-A2.

PD 16-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201; DB 5; Length 24292;
 Best Local Similarity 78.7%; Pred. No. 1.1e-46;
 RESULT 560
 ID AAK86316 standard; DNA; 25971 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41148.
 PN WO200157182-A2.

PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201; DB 4; Length 25971;
 Best Local Similarity 73.7%; Pred. No. 1.1e-46;
 RESULT 561
 ID AAB44338 standard; DNA; 34667 BP.
 DE Human transporter gene.
 PN WO2002408367-A2.

PA (SAGR-) SAGRES DISCOVERY INC. Query Match 22.2%; Score 201; DB 6; Length 34667;
 Best Local Similarity 81.4%; Pred. No. 1.2e-46;
 RESULT 562
 ID ABD33084 standard; DNA; 39699 BP.
 DE Human cancer-associated (CA) gene HD07-004.
 PN WO2004058146-A2.

PD 15-JUL-2004. PA (SAGR-) SAGRES DISCOVERY INC. Query Match 22.2%; Score 201; DB 13; Length 39699;

Best Local Similarity 81.4%; Pred. No. 1.3e-46;
 RESULT 563
 ID ACTN45050 standard; DNA; 41965 BP.
 DE Human Genomic sequence HCG39344.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.2%; Score 201; DB 11; Length 41966;
 Best Local Similarity 83.9%; Pred. No. 1.3e-46;
 RESULT 564
 ID AB68262 standard; DNA; 62944 BP.
 DE Kidney cancer related gene sequence SEQ ID NO:6599.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 22.2%; Score 201; DB 6; Length 62944;
 Best Local Similarity 78.7%; Pred. No. 1.6e-46;
 RESULT 565
 ID AB66947 standard; DNA; 62944 BP.
 DE Lung cancer related gene sequence SEQ ID NO:5284.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 22.2%; Score 201; DB 6; Length 62944;
 Best Local Similarity 78.7%; Pred. No. 1.6e-46;
 RESULT 566
 ID ADL13941 standard; DNA; 125515 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #473.
 PN WO20030504166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 22.2%; Score 201; DB 10; Length 125515;
 Best Local Similarity 77.2%; Pred. No. 2e-46;
 RESULT 567
 ID ADC87620 standard; DNA; 144792 BP.
 DE Human GPCR related polynucleotide SEQ ID NO:2073.
 PN EP1270774-A2.
 PD 02-JAN-2003.
 PA (NADD-) NAT INST ADVANCED IND SCI & TECHNOLOGY INCUBATION.
 (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATION.
 Query Match 22.2%; Score 201; DB 10; Length 144792;
 Best Local Similarity 84.5%; Pred. No. 2.1e-46;
 RESULT 568
 ID ADL13850 standard; DNA; 180550 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #382.
 PN WO20030504166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 22.2%; Score 201; DB 10; Length 180550;
 Best Local Similarity 81.4%; Pred. No. 2.3e-46;
 RESULT 569
 ID AB280229 standard; DNA; 249999 BP.
 DE Human trandorin gene region genomic DNA SEQ ID NO:26.
 PN WO2003016502-A2.
 PD 27-FEB-2003.
 PA (MCIL-) MC LAUGHLIN RES INST.
 Query Match 22.2%; Score 201; DB 8; Length 249999;
 Best Local Similarity 81.4%; Pred. No. 2.6e-46;
 RESULT 570
 ID ADC87619 standard; DNA; 349981 BP.
 DE Human GPCR related polynucleotide SEQ ID NO:2072.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NADD-) NAT INST ADVANCED IND SCI & TECHNOLOGY INCUBATION.
 (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATION.
 Query Match 22.2%; Score 201; DB 10; Length 349981;
 Best Local Similarity 84.5%; Pred. No. 3e-46;
 RESULT 571
 ID ACH29888 standard; cDNA; 390 BP.
 DE Human testis cDNA #274.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMANC-) DRMANC R T.
 PA (LABA-) LABAT I.
 PA (STAC-) STACHE-CRAN B.
 ID ADB9093 standard; cDNA; 4421 BP.
 DE Human retinal pigment epithelial-derived factor (PEDF) genomic DNA #3.
 PN US2003096750-A1.
 PD 22-MAY-2003.
 PA (TOMBL-) TOMBRAN-TINK J.
 PA (STER-) STEELE F R.
 PA (CHAD-) CHADER G J.
 PA (BECE-) BECERRA S P.
 PA (JOHN-) JOHNSON L V.
 PA (RODR-) RODRIGUEZ I R.
 Query Match 22.1%; Score 200 8; DB 10; Length 4421;
 Best Local Similarity 80.7%; Pred. No. 6.4e-47;
 RESULT 572
 ID ABS57269 standard; DNA; 4421 BP.
 DE Partial Sequence #3 of genomic DNA encoding human PEDF.
 PN US6451763-B1.
 PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.
 Query Match 22.1%; Score 200 8; DB 10; Length 4421;
 Best Local Similarity 80.7%; Pred. No. 6.4e-47;
 RESULT 573
 ID AAK89727 standard; DNA; 22645 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3303.
 PN WO20015334-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200 8; DB 4; Length 22645;
 Best Local Similarity 79.9%; Pred. No. 1.2e-46;
 RESULT 574
 ID AAL05495 standard; DNA; 22645 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 8183.
 PN WO20015320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200 8; DB 4; Length 22645;
 Best Local Similarity 79.9%; Pred. No. 1.2e-46;
 RESULT 575
 ID AAL04985 standard; DNA; 22645 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 7673.
 PN WO20015520-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200 8; DB 4; Length 22645;
 Best Local Similarity 79.9%; Pred. No. 1.2e-46;
 RESULT 576
 ID ABL97878 standard; DNA; 22645 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2530.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200 8; DB 4; Length 22645;
 Best Local Similarity 79.9%; Pred. No. 1.2e-46;
 RESULT 578
 ID ABL96348 standard; DNA; 22645 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3000.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200 8; DB 4; Length 22645;
 Best Local Similarity 79.9%; Pred. No. 1.2e-46;
 RESULT 579
 ID AAK66931 standard; DNA; 30620 BP.
 DE Human immune haematopoietic antigen genomic sequence SEQ ID NO:21743.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 22.1%; Score 200.8; DB 4; Length 30620;
 Best Local Similarity 80.9%; Pred. No. 1.3e-46;
 RESULT 580
 ID ADA0200 standard; DNA; 96593 BP.
 DE Human RUNX1 carcinoma associated gene, SEQ ID NO:1118.
 PN WO200305716-A2.
 PD 17-JUL-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Best Local Similarity 85.8%; Pred. No. 2.1e-46;
 RESULT 581
 ID ADB72338 standard; DNA; 96593 BP.
 DE Human RUNX1 gene.
 PN WO2003008533-A2.

PD 30-JAN-2003.

PA (SAGR-) SAGRES DISCOVERY 22.1%; Score 200.8; DB 9; Length 96593;
 Best Local Similarity 85.8%; Pred. No. 2.1e-46;
 RESULT 582
 ID ADB95818 standard; DNA; 96593 BP.
 DE Human RUNX1 gene, genomic DNA sequence.
 PN WO2003039484-A2.

PD 15-MAY-2003.

PA (SAGR-) SAGRES DISCOVERY 22.1%; Score 200.8; DB 10; Length 96593;
 Best Local Similarity 85.8%; Pred. No. 2.1e-46;
 RESULT 583
 ID AAD16330 standard; DNA; 107820 BP.
 DE Human ATP-binding cassette transporter ABCC6 (MRP6) complementary gene.
 Query Match 22.1%; Score 200.8; DB 4; Length 107820;
 Best Local Similarity 84.9%; Pred. No. 2.2e-46;

RESULT 584
 ID ACP62733 standard; DNA; 172984 BP.
 DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:661.
 PN WO20030113531-A2.

PD 20-FEB-2003.

PA (EPID-) EPIBAUROS BIOTECHNOLOGIE AG.
 Query Match 22.1%; Score 200.8; DB 8; Length 172984;
 Best Local Similarity 84.9%; Pred. No. 2.6e-46;

RESULT 585
 ID ADB20848 standard; DNA; 172984 BP.
 DE MRP1 based cancer related nucleic acid SEQ ID NO:661.
 PN WO2003013533-A2.

PD 20-FEB-2003.

PA (EPID-) EPIBAUROS BIOTECHNOLOGIE AG.
 Query Match 22.1%; Score 200.8; DB 8; Length 172984;
 Best Local Similarity 84.9%; Pred. No. 2.6e-46;

RESULT 586
 ID ADB87937 standard; DNA; 172984 BP.
 DE Human UGT1A1 gene sequence SEQ ID NO:661.
 PN WO2003013536-A2.

PD 20-FEB-2003.

PA (EPID-) EPIBAUROS BIOTECHNOLOGIE AG.
 Query Match 22.1%; Score 200.8; DB 10; Length 172984;
 Best Local Similarity 84.9%; Pred. No. 2.6e-46;

RESULT 587
 ID ADB96920 standard; DNA; 172984 BP.
 DE Human MDR1 related DNA sequence SEQ ID NO:661.
 PN WO2003013537-A2.

PD 20-FEB-2003.

PA (EPID-) EPIBAUROS BIOTECHNOLOGIE AG.
 Query Match 22.1%; Score 200.8; DB 10; Length 172984;
 Best Local Similarity 84.9%; Pred. No. 2.6e-46;

RESULT 588
 ID ADB92111 standard; DNA; 172984 BP.
 DE Human MDR1 related DNA sequence SEQ ID NO:661.
 PN WO2003013535-A2.

PD 20-FEB-2003.

PA (EPID-) EPIBAUROS BIOTECHNOLOGIE AG.
 Query Match 22.1%; Score 200.8; DB 10; Length 172984;
 Best Local Similarity 84.9%; Pred. No. 2.6e-46;

RESULT 589
 ID ADG97167 standard; DNA; 176771 BP.

DE Human cancer associated sequence HD2-0B-009, SEQ ID 143.
 PN WO2004060304-A2.
 PD 22-JUL-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
 Best Local Similarity 75.9%; Pred. No. 2.6e-46;
 RESULT 590
 ID ACN44418 standard; DNA; 213040 BP.
 DE Human genomic sequence hCG41574.
 PN WO2003073826-A2.

PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY 22.1%; Score 200.8; DB 11; Length 213040;
 Best Local Similarity 83.3%; Pred. No. 2.8e-46;

RESULT 591
 ID AH51011 standard; DNA; 319608 BP.
 DE Human chromosome 13q31-q33 genomic nucleotide sequence.
 PN WO20058510-A2.

PD 05-OCT-2000.

PA (GEST-) GENSET.
 Query Match 22.1%; Score 200.8; DB 3; Length 319608;
 Best Local Similarity 84.7%; Pred. No. 3.3e-46;

RESULT 592
 ID AHS09301 standard; DNA; 319608 BP.
 DE Human schizophrenia associated gene 935030 and biallelic markers A1-A71.
 PN 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200.6; DB 4; Length 2821;
 Best Local Similarity 84.7%; Pred. No. 6.1e-47;

RESULT 593
 ID AHS32797 standard; DNA; 5668 BP.
 DE Human genomic DNA for novel endocrine antigen, SEQ ID NO:751.
 PN WO200155319-A2.

PD 05-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200.6; DB 4; Length 5668;
 Best Local Similarity 83.0%; Pred. No. 8e-47;

RESULT 595
 ID ARK42719 standard; DNA; 8094 BP.
 DE Genomic sequence #618 encoding novel human connective tissue polypeptide.
 PN WO200155343-A1.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200.6; DB 4; Length 8894;
 Best Local Similarity 81.2%; Pred. No. 9.5e-47;

RESULT 596
 ID ARB60815 standard; DNA; 8894 BP.
 DE Connective tissue related genomic DNA #618.
 PN US2003054375-A1.

PD 20-MAR-2003.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200.6; DB 9; Length 8894;
 Best Local Similarity 81.2%; Pred. No. 9.5e-47;

RESULT 597
 ID ADS36489 standard; DNA; 14902 BP.
 DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1703.
 PN WO200408303-A2.

PD 30-SEP-2004.

PA (APPL-) APPLERA CORP.
 Query Match 22.1%; Score 200.6; DB 13; Length 14902;
 Best Local Similarity 81.4%; Pred. No. 1.2e-46;

RESULT 598
 ID ACM45210 standard; DNA; 49680 BP.
 DE Human genomic sequence hCG37835.
 PN WO2003073826-A2.

PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.

PN US2004072235-A1.
 PD 15-APR-2004.
 PA (DAWS-) DAWSON R P.
 Query Match Best Local Similarity
 RESULT 618 ID AAI62664 standard; DNA; 21936 BP.
 DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 314.
 PN WO20015524-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 619 ID AAL05758 standard; DNA; 21936 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9446.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 620 ID AAL06119 standard; DNA; 21936 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 8807.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 621 ID ABL96884 standard; DNA; 21936 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3336.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 622 ID ABL15065 standard; DNA; 21936 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 8196.
 PN WO200159053-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 623 ID ABL172317 standard; cDNA; 26657 BP.
 DE Human transporter protein gene.
 PN WO200202615-A2.
 PD 10-JAN-2002.
 PA (APPL-) APPLERA CORP.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 624 ID ABD32649 standard; DNA; 102790 BP.
 DE Human cancer-associated genomic DNA HD13-036.
 PN WO200407430-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 625 ID ABD32811 standard; DNA; 161051 BP.
 DE Human cancer-associated genomic DNA HD16-063.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 626 ID ACM44626 standard; DNA; 175077 BP.
 DE Human genomic sequence hCG19724.
 PN WO2003073826-A2.

PD 12-SBP-2003.
 PA (SAGR-) SAGRES DISCOVERY
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 627 ID AAB5879 standard; DNA; 226475 BP.
 DE Human tumour suppressor gene, Lmt reverse complement DNA.
 PN WO200306669-A1.
 PD 14-AUG-2003.
 PA (HALL-) HALL INST MEDICAL RES WALTER & BLIZA.
 Query Match Best Local Similarity
 Best Local Similarity
 Best Local Similarity
 Best Local Similarity
 RESULT 628 ID ABK83497 standard; cDNA; 227968 BP.
 DE Human cDNA differentially expressed in granulocytic cells #68.
 PN WO200228993-A2.
 PD 11-APR-2002.
 PA (GBNE-) GENE LOGIC INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 629 ID ADQ18338 standard; DNA; 227968 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1357.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 630 ID ADG4105 standard; DNA; 601 BP.
 DE Human transporter protein encoding gene fragment #11.
 PN US2004191029-A1.
 PD 30-SEP-2004.
 PA (APPL-) APPLERA CORP.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 631 ID AAK71508 standard; DNA; 781 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26320.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 632 ID AAK71507 standard; DNA; 796 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26319.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 633 ID AAK86179 standard; DNA; 3141 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40991.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 634 ID AAK86178 standard; DNA; 3341 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40990.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity
 Best Local Similarity
 RESULT 635 ID AAK85916 standard; DNA; 4533 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40728.
 PN WO200157182-A2.
 PD 09-AUG-2001.

Query Match 22.1%; Score 200; DB 11; Length 125534;
 Best Local Similarity 82.2%; Pred. No. 3.4e-46;
 RESULT 654
 ID ACN4142 standard; DNA; 143973 BP.
 DE Human genomic sequence hc01646502.
 PN WO2003073026-A2.
 PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.1%; Score 200; DB 11; Length 143973;
 Best Local Similarity 78.5%; Pred. No. 3.6e-46;
 RESULT 655
 ID ABQ77400 standard; DNA; 174566 BP.
 DE Human ITGB3 DNA.
 PN WO2003016594-A2.
 PD 27-FEB-2003.

PA (VITI-) VITIVITY INC. 22.1%; Score 200.2; DB 8; Length 174566;
 Best Local Similarity 83.0%; Pred. No. 3.9e-46;
 RESULT 656
 ID ADL08118 standard; DNA; 174566 BP.
 DE Human gene associated with low HDL-C ITGB3.
 RESULT 657
 ID ACN44650 standard; DNA; 256157 BP.
 DE Human genomic sequence hcg38672.
 PN WO2003073896-A2.
 PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.1%; Score 200.2; DB 11; Length 174566;
 Best Local Similarity 83.0%; Pred. No. 3.9e-46;
 RESULT 658
 ID AAB3570 standard; DNA; 256157 BP.
 DE Human cancer-associated (CNA) gene HB07-114.
 PN WO2003058166-A2.
 PD 15-JUN-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.1%; Score 200.2; DB 13; Length 256157;
 Best Local Similarity 83.0%; Pred. No. 4.5e-46;
 RESULT 659
 ID ADP26258 standard; DNA; 1061 BP.
 DE C35 promoter and polyuracotide targeting method related human DNA #1.
 PN WO2003037933-A2.
 PD 06-MAY-2004.

PA (UYRP) UNTIV ROCHESTER.
 PA (ZAUD/) ZAUDERER M..
 PA (PAR1/) PARIS M..
 PA Query Match 22.1%; Score 200; DB 12; Length 1061;
 Best Local Similarity 81.3%; Pred. No. 6.3e-47;
 RESULT 660
 ID AAB26259 standard; DNA; 1107 BP.
 DE Human breast cancer associated C35 promoter.
 PN WO2004037933-A2.
 PD 06-MAY-2004.

PA (UYRP) UNTIV ROCHESTER.
 PA (ZAUD/) ZAUDERER M..
 PA (PAR1/) PARIS M..
 PA Query Match 22.1%; Score 200; DB 12; Length 1107;
 Best Local Similarity 81.3%; Pred. No. 6.4e-47;
 RESULT 661
 ID ABO83751 standard; cDNA; 1812 BP.
 DE Human nucleotide reductase 16.83 encoding cDNA SEQ ID NO:1.
 PN CN1347389-A.
 PD 05-MAY-2002.

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 Query Match 22.1%; Score 200; DB 6; Length 1812;
 Best Local Similarity 81.3%; Pred. No. 7.7e-47;
 RESULT 662
 ID ADQ26270 standard; DNA; 7401 BP.
 DE C35 promoter and polynucleotide targeting method related human DNA #12.

PN WO2004037933-A2.
 PD 06-MAY-2004.
 PA (UYRP) UNIV ROCHESTER.
 PA (ZAUD/) ZAUDERER M..
 PA (PAR1/) PARIS M..
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 PA Query Match 22.1%; Score 200; DB 8; Length 23434;
 Best Local Similarity 78.1%; Pred. No. 2.1e-46;
 RESULT 669
 ID ACC0503 standard; DNA; 23434 BP.
 DE Human histone deacetylase HDAC10 genomic DNA sequence, SEQ ID NO:4.
 PN WO2003014340-A2.
 PD 20-FEB-2003.

PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 PA Query Match 22.1%; Score 200; DB 10; Length 46649;
 Best Local Similarity 79.1%; Pred. No. 2.7e-46;
 RESULT 670
 ID ADP9015 standard; DNA; 46649 BP.
 DE Genomic DNA encoding human transporter protein.
 PA Query Match 22.1%; Score 200; DB 10; Length 46649;
 Best Local Similarity 79.1%; Pred. No. 2.7e-46;
 RESULT 671
 ID ACN45002 standard; DNA; 60430 BP.
 DE Human genomic sequence hc0333210.
 PN WO2003073896-A2.
 PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY. 22.1%; Score 200; DB 11; Length 60430;
 Best Local Similarity 80.9%; Pred. No. 3e-46;
 RESULT 673
 ID ABK9411 standard; DNA; 109906 BP.
 DE DNA encoding endothelin converting enzyme 1 (ECF-1) #1.
 PN WO200224777-A2.
 PD 28-MAR-2002.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Best Local Similarity 85.4%; Pred. No. 3.7e-46;
 RESULT 673
 ID ADL08112 standard; DNA; 109906 BP.
 DE Human gene associated with low HDL-C ECST.
 PN US200443389-A1.
 PD 04-MAR-2004.
 PA (VITR-) VITIVITY INC.
 Query Match 22.1%; Score 200; DB 12; Length 109906;
 Best Local Similarity 85.4%; Pred. No. 3.7e-46;
 RESULT 674
 ID ABD3806 standard; DNA; 653458 BP.
 DE Human cancer-associated genomic DNA HD16-059.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.1%; Score 200; DB 13; Length 110000;
 Best Local Similarity 75.0%; Pred. No. 3.7e-46;
 RESULT 675
 ID ACN44334 standard; DNA; 161334 BP.
 DE Human genomic hCC32959.
 PN WO2003073826-A2.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.1%; Score 200; DB 11; Length 161334;
 Best Local Similarity 85.4%; Pred. No. 4.3e-46;
 RESULT 676
 ID ABD3688 standard; DNA; 208700 BP.
 DE Human cancer-associated genomic DNA HD14-005.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.1%; Score 200; DB 13; Length 208700;
 Best Local Similarity 80.4%; Pred. No. 4.8e-46;
 RESULT 677
 ID ADL13684 standard; DNA; 247509 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #216.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCI-) INCITE GENOMICS INC.
 Query Match 22.1%; Score 200; DB 10; Length 247509;
 Best Local Similarity 81.3%; Pred. No. 5.1e-46;
 RESULT 678
 ID ADP71180 standard; DNA; 304905 BP.
 DE Human Endophilin 2 gene.
 PN WO2003031594-A2.
 PD 17-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 22.1%; Score 200; DB 11; Length 304905;
 Best Local Similarity 74.3%; Pred. No. 5.5e-46;
 RESULT 679
 ID AAA02015 standard; cDNA; 711 BP.
 DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2006.
 PN WO958675-A2.
 PD 18-NOV-1995.
 PA (CHIR-) CHIRON CORP.
 (HYSE-) HYSEQ INC.
 Query Match 22.0%; Score 199.8; DB 3; Length 711;
 Best Local Similarity 82.8%; Pred. No. 6.1e-47;
 RESULT 680
 ID ALI37239 standard; DNA; 2306 BP.
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 3604.
 PN WO200155367-A1.
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 4; Length 2306;
 Best Local Similarity 81.1%; Pred. No. 9.6e-47;
 RESULT 681
 ID ABX60227 standard; cDNA; 2306 BP.
 DE cDNA encoding novel human musculoskeletal system antigen #2571.
 PN US2002147140-A1.
 PD 10-OCT-2002.
 PA (ROSE-) ROSEN C A.
 PA (RUBE-) RUBEN S M.
 PA (BARA-) BARASH S C.
 Query Match 22.0%; Score 199.8; DB 8; Length 2312;
 Best Local Similarity 81.1%; Pred. No. 9.6e-47;
 RESULT 682
 ID ADJ3977 standard; DNA; 2306 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3604.
 PN US200400488-A1.
 PD 15-JUN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 12; Length 2306;
 Best Local Similarity 81.1%; Pred. No. 9.6e-47;
 RESULT 683
 ID AAL37240 standard; DNA; 2311 BP.
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 3605.
 PN WO200155367-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 4; Length 2311;
 Best Local Similarity 81.1%; Pred. No. 9.6e-47;
 RESULT 684
 ID ABX60228 standard; cDNA; 2311 BP.
 DE cDNA encoding novel human musculoskeletal system antigen #2572.
 PN US2002147140-A1.
 PD 10-OCT-2002.
 PA (ROSE-) ROSEN C A.
 PA (RUBE-) RUBEN S M.
 PA (BARA-) BARASH S C.
 Query Match 22.0%; Score 199.8; DB 8; Length 2311;
 Best Local Similarity 81.1%; Pred. No. 9.6e-47;
 RESULT 685
 ID ADJ30978 standard; DNA; 2311 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3605.
 PN US2004009488-A1.
 PD 15-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 12; Length 2311;
 Best Local Similarity 81.1%; Pred. No. 9.6e-47;
 RESULT 686
 ID ALI37241 standard; DNA; 2312 BP.
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 3606.
 PN WO200155367-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 4; Length 2312;
 Best Local Similarity 81.1%; Pred. No. 9.6e-47;
 RESULT 687
 ID ABX60229 standard; cDNA; 2312 BP.
 DE cDNA encoding novel human musculoskeletal system antigen #2573.
 PN US2002147140-A1.
 PD 10-OCT-2002.
 PA (ROSE-) ROSEN C A.
 PA (RUBE-) RUBEN S M.
 PA (BARA-) BARASH S C.
 Query Match 22.0%; Score 199.8; DB 8; Length 2312;
 Best Local Similarity 81.1%; Pred. No. 9.6e-47;
 RESULT 688
 ID ADJ30979 standard; DNA; 2312 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3606.
 PN US2004009488-A1.
 PD 15-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 12; Length 2312;
 Best Local Similarity 81.1%; Pred. No. 9.6e-47;

RESULT 689
ID ADQ24272 standard; DNA; 3364 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7092.
PN WO2004048338-A2.

PA (PROM-) PROTEIN DESIGN LABS INC.
Query Match 22.0%; Score 199.8; DB 12; Length 3364;
Best Local Similarity 80.9%; Pred. No. 1.1e-46;

RESULT 690
ID ARI61061 standard; cDNA; 3775 BP.
DE Human polynucleotide SEQ ID NO 5050.

PN WO200153312-A1.

PD 26-JUL-2001.

PA (HYSE-) HYSEQ INC.
Query Match 22.0%; Score 199.8; DB 4; Length 3775;
Best Local Similarity 83.3%; Pred. No. 1.2e-45;

RESULT 691
ID AAK74057 standard; DNA; 5024 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28869.
PN WO200157188-A2.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 4; Length 5024;
Best Local Similarity 83.4%; Pred. No. 1.3e-46;

RESULT 692
ID AAK74056 standard; DNA; 5024 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28868.
PN WO200157182-A2.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 4; Length 5024;
Best Local Similarity 83.4%; Pred. No. 1.3e-46;

RESULT 693
ID ADC86178 standard; DNA; 10102 BP.
DE Human GPCR gene SEQ ID NO:1331.

PN EP1270724-A2.

PD 02-JAN-2003.

PA (RAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 22.0%; Score 199.8; DB 10; Length 10102;
Best Local Similarity 86.2%; Pred. No. 1.7e-46;

RESULT 694
ID AAS27797 standard; DNA; 18449 BP.
DE DNA encoding novel signal transduction pathway protein, Seq ID 1457.
PN WO200154733-A1.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 4; Length 18449;
Best Local Similarity 80.9%; Pred. No. 2.1e-46;

RESULT 695
ID ABR20913 standard; DNA; 18449 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13244.

PN WO200159063-A2.

PD 16-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 5; Length 18449;
Best Local Similarity 80.9%; Pred. No. 2.1e-46;

RESULT 696
ID ADB94600 standard; DNA; 18449 BP.
DE Novel human protein DNA #209.
PN US2002168711-A1.

PD 14-NOV-2002.

PA (ROSE-) ROSEN C A.

PA (RUBR-) RUBEN S M.

PA (BARA/) BARASH S C.

Query Match 22.0%; Score 199.8; DB 10; Length 18449;
Best Local Similarity 80.9%; Pred. No. 2.1e-46;

RESULT 697
ID ACM44810 standard; DNA; 25668 BP.
DE Human genomic sequence hCG28302.
PN WO2003073826-A2.

PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.

Query Match 22.0%; Score 199.8; DB 11; Length 25668;
Best Local Similarity 80.9%; Pred. No. 2.4e-46;

RESULT 698
ID ABA07160 standard; DNA; 31931 BP.
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 479.

PN WO200152064-A1.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 4; Length 31931;
Best Local Similarity 83.3%; Pred. No. 2.6e-46;

RESULT 699
ID ADC0666 standard; DNA; 51961 BP.
DE Human secreted protein-related DNA sequence #84.

PN WO2002912787-A2.

PD 21-NOV-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 10; Length 51961;
Best Local Similarity 83.3%; Pred. No. 3.2e-46;

RESULT 700
ID ABT16005 standard; DNA; 51961 BP.
DE Human secreted protein-related DNA sequence - SEQ ID NO 259.

PN WO2002217188-A2.

PD 03-OCT-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 10; Length 51961;
Best Local Similarity 83.3%; Pred. No. 3.2e-46;

RESULT 701
ID AB267188 standard; DNA; 51961 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1011.

PN WO20027186-A2.

PD 03-OCT-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 10; Length 51961;
Best Local Similarity 83.3%; Pred. No. 3.2e-46;

RESULT 702
ID ABE95902 standard; DNA; 94719 BP.
DE Human STAT5B gene genomic DNA sequence.

PN WO2003039484-A2.

PD 15-MAY-2003.

PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.8; DB 10; Length 94719;
Best Local Similarity 81.1%; Pred. No. 4e-46;

RESULT 703
ID ADA02654 standard; DNA; 94720 BP.
DE Human STAT5B carcinoma associated gene, SEQ ID NO:1172.

PN WO2003035714-A2.

PD 17-JUL-2003.

PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.8; DB 9; Length 94720;
Best Local Similarity 81.1%; Pred. No. 4e-46;

RESULT 704
ID ADB72392 standard; DNA; 94720 BP.
DE Human STAT5B gene.

PN WO200310853-A2.

PD 30-JAN-2003.

PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.8; DB 10; Length 94720;
Best Local Similarity 81.1%; Pred. No. 4e-46;

RESULT 705
ID ADO97846 standard; DNA; 94911 BP.
DE Human cancer associated sequence HD11-010, SEQ ID 823.

PN WO2004060304-A2.

PD 22-JUL-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.0%; Score 199.8; DB 12; Length 94911;
Best Local Similarity 79.7%; Pred. No. 4e-46;

RESULT 706
ID ADM06353 standard; DNA; 398800 BP.
DE Human FLAP genomic DNA SEQ ID NO:1.
PN WO0401035741-A2.

PD 29-APR-2004.

PA (DECO-) DECODE GENETICS BHF.
Query Match 22.0%; Score 199.8; DB 12; Length 110000;

Best Local Similarity 80.9%; Pred. No. 4.3e-46; RESULT 707
ID ADS94372 standard; DNA; 398800 BP.
DE Human 5-lipoxygenase activating protein (FLAP) gene.
PN WO2004035746-A2.
PD 29-APR-2004.
PA (DECO-) DECODE GENETICS EHF.
Query Match 22.0%; Score 199.8; DB 13; Length 110000;
Best Local Similarity 80.9%; Pred. No. 4.3e-46;
RESULT 708
ID ACM44026 standard; DNA; 122923 BP.
DE Human genomic sequence hCG24510.
PN WO2003073626-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.8; DB 11; Length 122923;
Best Local Similarity 80.9%; Pred. No. 4.5e-46;
RESULT 709
ID ADQ21602 standard; DNA; 131673 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4422.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.0%; Score 199.8; DB 12; Length 131673;
Best Local Similarity 84.6%; Pred. No. 4.6e-46;
RESULT 710
ID ADQ19389 standard; DNA; 155937 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2208.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.0%; Score 199.8; DB 12; Length 155937;
Best Local Similarity 83.0%; Pred. No. 4.9e-46;
RESULT 711
ID AAD05697 standard; DNA; 16052 BP.
DE Human glycosyl sulfotransferase-4 (GST-4) genomic DNA.
PN WO200106015-A1.
PD 25-JAN-2001.
PA (REGC-) UNIV CALIFORNIA.
Query Match 22.0%; Score 199.8; DB 4; Length 16052;
Best Local Similarity 76.7%; Pred. No. 4.9e-46;
RESULT 712
ID ABD3314 standard; DNA; 170489 BP.
DE Human cancer-associated (CA) gene HD07-056.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.0%; Score 199.8; DB 13; Length 170489;
Best Local Similarity 80.9%; Pred. No. 5.1e-46;
RESULT 713
ID ACN43946 standard; DNA; 174448 BP.
DE Human genomic sequence hCG21793.
PN WO2003073626-A2.
PD 20-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.8; DB 11; Length 174448;
Best Local Similarity 82.0%; Pred. No. 5.1e-46;
RESULT 714
ID ADE09750 standard; DNA; 1608 BP.
DE Novel DNA-related contig nucleotide sequence #472.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 22.0%; Score 199.6; DB 10; Length 1608;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 715
ID ADS11591 standard; DNA; 1608 BP.
DE Human therapeutic contig DNA - SEQ ID 1828.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 1608;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 716
ID ADS1159 standard; DNA; 1608 BP.
DE Human therapeutic contig DNA - SEQ ID 1829.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 1608;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 717
ID ADS1159 standard; DNA; 1608 BP.
DE Human therapeutic contig DNA - SEQ ID 1827.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 1608;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 718
ID ADS1159 standard; DNA; 1608 BP.
DE Human therapeutic contig DNA - SEQ ID 1396.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 1608;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 719
ID AAK9819 standard; cDNA; 1748 BP.
DE Human full-length cDNA; SEQ ID NO: 3960.
PN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 22.0%; Score 199.6; DB 4; Length 1748;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 720
ID ADJ1927 standard; cDNA; 1748 BP.
DE Full length human cDNA clone SeqID 3960.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RFS ASSOC BIOTECHNOLOGY.
Query Match 22.0%; Score 199.6; DB 12; Length 1748;
Best Local Similarity 84.1%; Pred. No. 9.9e-47;
RESULT 721
ID ADA5479 standard; cDNA; 2261 BP.
DE Human coding sequence; SEQ ID 47.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
Query Match 22.0%; Score 199.6; DB 10; Length 2261;
Best Local Similarity 84.1%; Pred. No. 1.1e-46;
RESULT 722
ID AA159666 standard; cDNA; 2982 BP.
DE Human polynucleotide SEQ ID NO 3655.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.0%; Score 199.6; DB 4; Length 2982;
Best Local Similarity 84.1%; Pred. No. 1.2e-46;
RESULT 723
ID ABK69113 standard; cDNA; 3047 BP.
DE DNA encoding human secreted protein; SEQ ID NO 37.
PN WO200224721-A1.
PD 28-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 6; Length 3047;
Best Local Similarity 84.1%; Pred. No. 1.2e-46;
RESULT 724
ID AA157880 standard; cDNA; 3262 BP.
DE Human polynucleotide SEQ ID NO 83.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.0%; Score 199.6; DB 4; Length 3262;
Best Local Similarity 84.1%; Pred. No. 1.3e-46;

RESULT 725
ID ADQ67504 standard; cDNA; 3660 BP.
DE Novel human cDNA sequence #2477.
PN EP1440981-A2.
RESULT 726
ID ABQ81341 standard; cDNA; 3716 BP.
DE Human PMM encoding sequence Incyte ID 7372712CB1.
PN WO200246383-A2.
PD 13-JUN-2002.
ID (INCY-) INCYTE GENOMICS INC.
DE Best Local Similarity 84.1%; Pred. No. 1.3e-46;
PN Query Match 22.0%; Score 199.6; DB 12; Length 3660;
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity 84.0%; Score 199.6; DB 12; Length 3660;
PA (FERR) FERRING BV.
Best Local Similarity 84.1%; Pred. No. 1.3e-46;
PN ABK81341 standard; cDNA; 3716 BP.
DE cDNA encoding human DPRP-2 splice variant #9.
PD 18-APR-2002.
ID (FERR) FERRING BV.
Best Local Similarity 84.1%; Pred. No. 1.3e-46;
PN ABK81341 standard; cDNA; 3716 BP.
DE cDNA encoding human DPRP-2 splice variant #9.
PD 18-APR-2002.
ID (FERR) FERRING BV.
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
PN ABK81337 standard; cDNA; 4076 BP.
DE cDNA encoding human DPRP-2 splice variant #5.
PN WO200231134-A2.
ID ABK81340 standard; cDNA; 4120 BP.
DE cDNA encoding human DPRP-2 splice variant #8.
PN WO200231134-A2.
ID (FERR) FERRING BV.
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
PN ABQ86753 standard; cDNA; 4147 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3628.
PN WO2004060270-A2.
PD 22-JUL-2004.
ID (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 22.0%; Score 199.6; DB 12; Length 4147;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 731
ID ADQ84273 standard; cDNA; 4147 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1087.
PN WO2004060270-A2.
PD 22-JUL-2004.
ID (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 22.0%; Score 199.6; DB 13; Length 4147;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 732
ID ACM40423 standard; cDNA; 4147 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326538, SEQ ID NO:5194.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 4147;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 733
ID AAK79133 standard; DNA; 14216 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33943.
PN WO2004030615-A2.
ID AAK79133 standard; DNA; 14216 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33945.
PN WO2004030615-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 4; Length 14216;
Best Local Similarity 84.1%; Pred. No. 2.2e-46;
RESULT 742
ID AAK79131 standard; DNA; 14216 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33943.
PN WO2004030615-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 22.0%; Score 199.6; DB 4; Length 14216;
 Best Local Similarity 84.1%; Pred. No. 2.2e-46;
 RESULT 743
 ID ASN41759 Standard; DNA; 22428 BP.
 DE Genomic sequence #75 encoding novel human enzyme polypeptide.
 PN WO200155301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.6; DB 4; Length 22428;
 Best Local Similarity 84.1%; Pred. No. 2.6e-46;
 RESULT 744
 ID ABZ7401 Standard; DNA; 22428 BP.
 DE Secreted protein gene 215 genomic fragment HNGAM5B, SEQ ID NO:1348.
 PN WO200277018-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.6; DB 8; Length 22428;
 Best Local Similarity 84.1%; Pred. No. 2.6e-46;
 RESULT 745
 ID ADA98730 Standard; DNA; 22428 BP.
 DE Human secreted protein-related DNA sequence #323.
 PN WO2003004623-A2.
 PD 16-JAN-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.6; DB 8; Length 22428;
 Best Local Similarity 84.1%; Pred. No. 2.6e-46;
 RESULT 746
 ID ABZ67767 Standard; DNA; 22428 BP.
 DE Human secreted protein encoding genomic DNA SEQ ID NO 1290.
 PN WO200377186-A2.
 PD 03-OCT-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.6; DB 10; Length 22428;
 Best Local Similarity 84.1%; Pred. No. 2.6e-46;
 RESULT 747
 ID AAK81763 Standard; DNA; 37959 BP.
 DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:36575.
 PN WO200315182-A2.
 PD 09-AUG-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.6; DB 4; Length 37959;
 Best Local Similarity 82.8%; Pred. No. 3.2e-46;
 RESULT 748
 ID ACN44819 Standard; DNA; 116704 BP.
 DE Human genomic sequence hCG30155.
 PN WO2003073926-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.0%; Score 199.6; DB 11; Length 116704;
 Best Local Similarity 82.9%; Pred. No. 5e-46;
 RESULT 749
 ID ADP80536 Standard; DNA; 118788 BP.
 DE Human HPC2/ELAC2 gene SeqID1.
 PN JP2004166365-A.
 PD 17-JUN-2004.
 PA (TAKA-) TAKAHASHI H.
 PA (WATA-) WATANABE M.
 PA (FURU-) FURUSATO M.
 PA (HONS-) YAKULT HONSHA KK.
 Query Match 22.0%; Score 199.6; DB 12; Length 118788;
 Best Local Similarity 82.8%; Pred. No. 5e-46;
 RESULT 750
 ID ABD3219 Standard; DNA; 135827 BP.
 DE Human cancer-associated (CA) gene HD07-035.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.0%; Score 199.6; DB 13; Length 135827;
 Best Local Similarity 78.6%; Pred. No. 5.3e-46;
 RESULT 751
 ID ABD2612 Standard; DNA; 142976 BP.
 DE Human cancer-associated genomic DNA HD12-017.
 PN WO2004074320-A2.

PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.0%; Score 199.6; DB 13; Length 142976;
 Best Local Similarity 83.1%; Pred. No. 5.4e-46;
 RESULT 752
 ID ACN44374 Standard; DNA; 181684 BP.
 DE Human genomic sequence hCG16651.
 PN WO2003073826-A2.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.0%; Score 199.6; DB 11; Length 181684;
 Best Local Similarity 82.8%; Pred. No. 5.9e-46;
 RESULT 753
 ID AH92610 Standard; DNA; 700 BP.
 DE Human inflammatory bowel disease related gene fragment IGR1310a.
 PN WO200142511-A2.
 PD 14-JUN-2001.
 PA (WHED-) WHITEHEAD INST BIOMEDICAL RES.
 PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
 Query Match 22.0%; Score 199.4; DB 4; Length 700;
 Best Local Similarity 81.1%; Pred. No. 7.9e-47;
 RESULT 754
 ID AAL36476 Standard; DNA; 1664 BP.
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 2841.
 PN WO200153367-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.4; DB 4; Length 1664;
 Best Local Similarity 86.4%; Pred. No. 1.1e-46;
 RESULT 755
 ID ABX5464 Standard; cDNA; 1664 BP.
 DE cDNA encoding novel human musculoskeletal system antigen #1808.
 PN US2002147140-A1.
 PD 10-OCT-2002.
 PA (ROSE-) ROSEN C A.
 PA (RUBE-) RUBEN S M.
 PA (BARA-) BARASH S C.
 Query Match 22.0%; Score 199.4; DB 8; Length 1664;
 Best Local Similarity 86.4%; Pred. No. 1.1e-46;
 RESULT 756
 ID ADJ30214 Standard; DNA; 1664 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2841.
 PN US2004009488-A1.
 PD 15-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.4; DB 12; Length 1664;
 Best Local Similarity 86.4%; Pred. No. 1.1e-46;
 RESULT 757
 ID ADM03474 Standard; cDNA; 1756 BP.
 DE Human CDNA of the invention SEQ ID NO:2159.
 PN EP1347046-A1.
 PD 24-SEP-2003.
 PA (REAC-) REES ASSOC BIOTECHNOLOGY.
 Query Match 22.0%; Score 199.4; DB 11; Length 1756;
 Best Local Similarity 82.4%; Pred. No. 1.1e-46;
 RESULT 758
 ID ABK9513 Standard; DNA; 6096 BP.
 DE Human prostate specific nucleic acid #132.
 PN WO200338810-A2.
 PD 16-MAY-2002.
 PA (DIAD-) DIADEXUS INC.
 Query Match 22.0%; Score 199.4; DB 6; Length 6096;
 Best Local Similarity 76.0%; Pred. No. 1.8e-46;
 RESULT 759
 ID AAS42014 Standard; DNA; 6437 BP.
 DE Genomic sequence #330 encoding novel human enzyme polypeptide.
 PN WO200155301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.4; DB 4; Length 6437;
 Best Local Similarity 81.1%; Pred. No. 1.9e-46;
 RESULT 760
 ID AAK69231 Standard; DNA; 8658 BP.

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24043.	PD 27-NOV-2003.
PN WO200515182-A2.	PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PD 09-AUG-2001.	Query Match 22.0%; Score 199.4; DB 12; Length 124167;
PA (HUMA-) HUMAN GENOME SCI INC.	Best Local Similarity 81.1%; Pred. No. 5.8e-46;
RESULT 761	RESULT 771
ID AS42015 standard; DNA; 9742 BP.	ID ADQ9701 standard; DNA; 12722 BP.
DE Genomic sequence #331 encoding novel human enzyme polypeptide.	DE Human cancer associated sequence HD08-028, SEQ ID 278.
PN WO2005153012-A2.	PN WO2004060304-A2.
PD 02-AUG-2001.	PD 22-JUL-2004.
PA (HUMA-) HUMAN GENOME SCI INC.	PA (SAGR-) SACRES DISCOVERY INC.
Query Match 22.0%; Score 199.4; DB 4; Length 9742;	Query Match 22.0%; Score 199.4; DB 12; Length 127722;
Best Local Similarity 81.1%; Pred. No. 2.2e-46;	Best Local Similarity 81.5%; Pred. No. 5.9e-46;
RESULT 762	RESULT 772
ID ACN4990 standard; DNA; 33317 BP.	ID AD5538 standard; DNA; 133893 BP.
DE Human genomic sequence hCG7461.	DE Human Phosphatidylinositol biphosphate (PIB) DNA #1.
PN WO2005073826-A2.	PN WO200519121-A1.
PD 12-SEP-2003.	PD 12-DEC-2002.
PA (SAGR-) SACRES DISCOVERY.	PA (EXEL-) EXALIXIS INC.
Query Match 22.0%; Score 199.4; DB 11; Length 33317;	Query Match 22.0%; Score 199.4; DB 9; Length 133893;
Best Local Similarity 81.3%; Pred. No. 3.5e-46;	Best Local Similarity 78.9%; Pred. No. 6e-46;
RESULT 763	RESULT 773
ID AAD44395 standard; DNA; 49984 BP.	ID ADL13338 standard; DNA; 186528 BP.
DE Human transporter genomic DNA.	DE Osteoarthritis-associated polymorphic nucleotide #170.
RESULT 764	DN WO2005054166-A2.
ID ADS6492 standard; DNA; 49984 BP.	DN 03-JUL-2003.
DE Human transporter protein encoding gene.	PA (INCY-) INCYTB GENOMICS INC.
Query Match 22.0%; Score 199.4; DB 13; Length 49984;	Query Match 22.0%; Score 199.4; DB 10; Length 186528;
Best Local Similarity 81.1%; Pred. No. 4.1e-46;	Best Local Similarity 79.9%; Pred. No. 6.8e-46;
RESULT 765	RESULT 774
ID AAL53466 standard; DNA; 70372 BP.	ID ABD3298 standard; DNA; 290547 BP.
DE Rab-like protein genomic DNA.	DE Human cancer-associated genomic DNA HD7-220.
Query Match 22.0%; Score 199.4; DB 6; Length 70372;	DN WO2004074320-A2.
Best Local Similarity 81.1%; Pred. No. 4.7e-46;	PD 02-SEP-2004.
RESULT 766	PA (SAGR-) SACRES DISCOVERY INC.
ID ADQ97870 standard; DNA; 121160 BP.	Query Match 22.0%; Score 199.4; DB 13; Length 290547;
DE Human cancer associated sequence HD11-015, SEQ ID 847.	Best Local Similarity 81.1%; Pred. No. 8.1e-46;
PN WO2004060304-A2.	RESULT 775
PD 22-JUL-2004.	ID ABX61843 standard; DNA; 601 BP.
PA (SAGR-) SACRES DISCOVERY INC.	DS Novel human transporter protein related polymucleotide #39.
Query Match 22.0%; Score 199.4; DB 12; Length 121160;	DN US2002142381-A1.
Best Local Similarity 76.0%; Pred. No. 5.8e-46;	PD 03-OCT-2002.
RESULT 767	PA (CONG-) CONG F.
ID AHD19244 standard; DNA; 121464 BP.	PA (KETC-) KETCHUM K A.
DE Human 5-hydroxytryptamine receptor type 3B SNP variant DNA.	PA (DFRA-) DI FRANCESCO V.
PN WO2003097873-A2.	PA (BRAS-) BEASLEY E M.
PD 27-NOV-2003.	Query Match 22.0%; Score 199.2; DB 8; Length 601;
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.	Best Local Similarity 76.7%; Pred. No. 8.5e-47;
Query Match 22.0%; Score 199.4; DB 12; Length 124164;	RESULT 776
Best Local Similarity 81.1%; Pred. No. 5.8e-46;	ID AAK80126 standard; DNA; 4115 BP.
RESULT 768	DB Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34938.
ID AHD19246 standard; DNA; 124165 BP.	DN WO200517182-A2.
DE Human 5-hydroxytryptamine receptor type 3B SNP variant DNA 2.	PD 03-AUG-2001.
PN WO2003097873-A2.	PA (HUMA-) HUMAN GENOME SCI INC.
PD 27-NOV-2003.	Query Match 22.0%; Score 199.2; DB 4; Length 4115;
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.	Best Local Similarity 84.6%; Pred. No. 1.8e-46;
Query Match 22.0%; Score 199.4; DB 12; Length 124165;	RESULT 777
Best Local Similarity 81.1%; Pred. No. 5.8e-46;	ID ABQ78002 standard; DNA; 21222 BP.
RESULT 769	DE Human transporter protein encoding genomic DNA SEQ ID NO 3.
ID ADP83402 standard; DNA; 124167 BP.	Query Match 22.0%; Score 199.2; DB 6; Length 21222;
DE Human 5-hydroxytryptamine receptor type 3 gene.	Best Local Similarity 80.6%; Pred. No. 3.4e-46;
PN WO200310091-A1.	RESULT 778
PD 04-DEC-2003.	ID AAK89418 standard; DNA; 20588 BP.
PA (HUMA-) EPIDAUROS BIOTECHNOLOGIE AG.	DE Human digestive system antigen genomic sequence SEQ ID NO: 2994.
Query Match 22.0%; Score 199.4; DB 12; Length 124167;	DN WO2001015314-A2.
Best Local Similarity 81.1%; Pred. No. 5.8e-46;	PD 03-AUG-2001.
RESULT 770	PA (HUMA-) HUMAN GENOME SCI INC.
ID ADH19240 standard; DNA; 124167 BP.	Query Match 22.0%; Score 199.2; DB 4; Length 28588;
DE Human 5-hydroxytryptamine receptor type 3B gDNA.	Best Local Similarity 82.8%; Pred. No. 3.8e-46;
PN WO2003097873-A2.	RESULT 779
PD 02-AUG-2001.	ID AAK831923 standard; DNA; 28588 BP.
PA (HUMA-) EPIDAUROS BIOTECHNOLOGIE AG.	DE Human liver associated genomic DNA #97.
Query Match 22.0%; Score 199.4; DB 12; Length 124167;	DN WO2001015355-A1.
Best Local Similarity 81.1%; Pred. No. 5.8e-46;	PD 02-AUG-2001.
RESULT 770	
ID ADH19240 standard; DNA; 124167 BP.	
DE Human 5-hydroxytryptamine receptor type 3B gDNA.	
PN WO2003097873-A2.	

PA (RHUMA-) HUMAN GENOME SCI INC. Query Match 22.0%; Score 199.2; DB 5; Length 28588; Best Local Similarity 82.8%; Pred. No. 3.8e-46; RESULT 780 ID ABN90278 standard; DNA; 28588 BP. DE Human liver antigen HLR194 genomic sequence, SEQ ID NO:399. PN US20030420056-A1.

PA (ROSE/) ROSEN C A. (RUBE/) RUBEN S M. (BARA-) BARASH S C. PD 24-APR-2003. Query Match 22.0%; Score 199.2; DB 6; Length 28588; Best Local Similarity 82.8%; Pred. No. 3.8e-46; RESULT 781 ID ADJ15191 standard; DNA; 25888 BP. DE Human liver-related genomic DNA - SEQ ID 399. PN US2003077602-A1.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 22.0%; Score 199.2; DB 11; Length 28588; Best Local Similarity 82.8%; Pred. No. 3.8e-46; RESULT 782 ID ABD8217 standard; DNA; 30709 BP. DE Human lipase, hormone-sensitive (LIPB) gene sequence. Best Local Similarity 83.0%; Pred. No. 3.9e-46; RESULT 783 ID ABD33578 standard; DNA; 43853 BP. DE Human cancer-associated (CA) gene HD07-116. PN WO200405816-A2. PD 15-JUL-2004.

PA (SAGR-) SAGRES DISCOVERY INC. Query Match 22.0%; Score 199.2; DB 13; Length 43853; Best Local Similarity 80.6%; Pred. No. 4.5e-46; RESULT 784 ID ACN43885 standard; DNA; 61103 BP. DE Human genomic sequence hCG1784975. PN WO2003073826-A2.

PA (SAGR-) SAGRES DISCOVERY. Query Match 22.0%; Score 199.2; DB 11; Length 61103; Best Local Similarity 81.9%; Pred. No. 5.1e-46; RESULT 785 ID ACN44230 standard; DNA; 66973 BP. DE Human genomic sequence hCG21559. PN WO2003073826-A2.

PA 12-SEP-2003. Query Match 22.0%; Score 199.2; DB 11; Length 66973; Best Local Similarity 84.4%; Pred. No. 5.2e-46; RESULT 786 ID ADQ97368 standard; DNA; 78082 BP. DE Human cancer associated sequence HD11-032, SEQ ID 945. PN WO2004050304-A2. PD 22-JUL-2004.

PA (SAGR-) SAGRES DISCOVERY INC. Query Match 22.0%; Score 199.2; DB 12; Length 78082; Best Local Similarity 82.8%; Pred. No. 5.6e-46; RESULT 787 Query Match 22.0%; Score 199.2; DB 13; Length 88759; Best Local Similarity 80.1%; Pred. No. 5.8e-46; RESULT 788 ID ADH56139 standard; DNA; 95001 BP. DE Human hypothetical tumour endothelial marker DNA. PN US2003232770-A1.

PA (ISIS-) ISIS PHARM INC. Query Match 22.0%; Score 199.2; DB 12; Length 95001; Best Local Similarity 80.6%; Pred. No. 6e-46; RESULT 789 ID ADC83301 standard; DNA; 96591 BP. DE Mouse Sos1 coding sequence. PN WO2003045230-A2.

PA (SAGR-) SAGRES DISCOVERY INC. Query Match 22.0%; Score 199.2; DB 10; Length 96591; Best Local Similarity 76.0%; Pred. No. 6e-46; RESULT 790 ID ADA02822 standard; DNA; 96592 BP. DE Human SOS1 carcinoma associated gene, SEQ ID NO:1340. PN WO2003057146-A2.

PA (SAGR-) SAGRES DISCOVERY. Query Match 22.0%; Score 199.2; DB 9; Length 96592; Best Local Similarity 75.0%; Pred. No. 6e-46; RESULT 791 ID ADB72560 standard; DNA; 96592 BP. DE Human SOS1 gene. PN WO2003008583-A2.

PA 30-JAN-2003. PA (SAGR-) SAGRES DISCOVERY. Query Match 22.0%; Score 199.2; DB 10; Length 96592; Best Local Similarity 76.0%; Pred. No. 6e-46; RESULT 792 ID ADM74417 standard; DNA; 96592 BP. DE Human carcinoma associated (CA) nucleic acid #43. PN US2004072154-A1. PD 15-APR-2004.

PA (MORR/) MORRIS D W. (ENGEL/) ENGELHARD E K. Query Match 22.0%; Score 199.2; DB 12; Length 96592; Best Local Similarity 76.0%; Pred. No. 6e-46; RESULT 793 ID ADS3661 standard; DNA; 158417 BP. DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1675. PN WO200408183-A2.

PA (APPL-) APPLERA CORP. Query Match 22.0%; Score 199.2; DB 13; Length 158417; Best Local Similarity 85.1%; Pred. No. 7.3e-46; RESULT 794 ID AH11291 standard; cDNA; 559 BP. DE Human cDNA clone (3'-primer) SEQ ID NO:10126. PN EP1074617-A2.

PA (HELI-) HELIX RBS INST. Query Match 21.9%; Score 199; DB 4; Length 559; Best Local Similarity 83.8%; Pred. No. 9.5e-47; RESULT 795 ID AAK72318 standard; DNA; 2502 BP. DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27330. PN WO2003157182-A2. PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.9%; Score 199; DB 4; Length 2502; Best Local Similarity 85.1%; Pred. No. 1.7e-46; RESULT 796 ID AAK70822 standard; DNA; 3371 BP. DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25634. PN WO2003157182-A2.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.9%; Score 199; DB 4; Length 3371; Best Local Similarity 78.0%; Pred. No. 1.9e-46; RESULT 797 ID ADQ64445 standard; cDNA; 4634 BP. DE Novel human cDNA sequence #2006. PN EP1449981-A2.

PA (REAS-) RES ASSOC BIOTECHNOLOGY. Query Match 21.9%; Score 199; DB 12; Length 4634; Best Local Similarity 85.1%; Pred. No. 2.1e-46; RESULT 798 ID ABA2057 standard; DNA; 11234 BP. DE Human nervous system related polynucleotide SEQ ID NO 13188. PN WO200159063-A2.

PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 199; DB 5; Length 11234;
 Best Local Similarity 81.3%; Pred. No. 3e-46;
 RESULT 799
 ID ABK49701 standard; DNA; 32816 BP.
 DE Human transporter protein genomic DNA sequence.
 Query Match 21.9%; Score 199; DB 6; Length 32816;
 Best Local Similarity 85.1%; Pred. No. 4.5e-46;
 RESULT 800
 ID ADG16994 standard; DNA; 32816 BP.
 DR Human transporter protein DNA.
 Query Match 21.9%; Score 199; DB 12; Length 32816;
 Best Local Similarity 85.1%; Pred. No. 4.5e-46;
 RESULT 801
 ID ABX13675 standard; DNA; 33239 BP.
 DR Human Secreted protein gene.
 PN US200213710-A1.
 PD 26-SEP-2002.
 PA (NBIM/) WEI M.
 PA (GONG/) GONG F.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS-) BEASLEY E M.
 Query Match 21.9%; Score 199; DB 8; Length 33239;
 Best Local Similarity 81.5%; Pred. No. 4.6e-46;
 RESULT 802
 ID AAK74751 standard; DNA; 36485 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29563.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 DR Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23770.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 199; DB 4; Length 36485;
 Best Local Similarity 80.1%; Pred. No. 4.7e-46;
 RESULT 803
 ID AAK68958 standard; DNA; 36485 BP.
 DR Human genome standard; DNA; 36485 BP.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.9%; Score 199; DB 4; Length 36485;
 Best Local Similarity 80.1%; Pred. No. 4.7e-46;
 RESULT 804
 ID AAK68958 standard; DNA; 36485 BP.
 DR Human enzyme protein encoding gene.
 Query Match 21.9%; Score 199; DB 8; Length 39982;
 Best Local Similarity 85.1%; Pred. No. 4.9e-46;
 RESULT 805
 ID ABD32585 standard; DNA; 50927 BP.
 DR Human cancer-associated genomic DNA HD7-210.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.9%; Score 199; DB 13; Length 50927;
 Best Local Similarity 85.1%; Pred. No. 5.4e-46;
 RESULT 806
 ID ABD32585 standard; DNA; 106130 BP.
 DR Human cancer associated sequence HD10-012, SEQ ID 576.
 PN WO2004050304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.9%; Score 199; DB 12; Length 106130;
 Best Local Similarity 85.1%; Pred. No. 7.1e-46;
 RESULT 807
 DR Human genomic sequence hCG1781402.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.9%; Score 199; DB 11; Length 126266;
 Best Local Similarity 81.5%; Pred. No. 7.6e-46;

RESULT 809
 ID ADH63063 standard; DNA; 132762 BP.
 DE Human fibroblast growth factor receptor 2 related sequence, SEQ ID 17.
 PN WO2003024987-A1.
 PD 27-MAR-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.9%; Score 199; DB 10; Length 132762;
 Best Local Similarity 81.5%; Pred. No. 7.8e-46;
 RESULT 810
 ID ADP45544 standard; DNA; 133100 BP.
 DE Human NUMA1/FLJ20625/LOC220074 region gDNA.
 Query Match 21.9%; Score 199; DB 12; Length 133100;
 Best Local Similarity 81.5%; Pred. No. 7.8e-46;
 RESULT 811
 ID ACM62841 standard; DNA; 148567 BP.
 DE Human kinase DNA.
 Query Match 21.9%; Score 199; DB 9; Length 148567;
 Best Local Similarity 79.3%; Pred. No. 8.1e-46;
 RESULT 812
 ID AB55500 standard; DNA; 148567 BP.
 DE Gene encoding human Serine/threonine protein kinase-like kinase.
 Query Match 21.9%; Score 199; DB 10; Length 148567;
 Best Local Similarity 79.3%; Pred. No. 8.1e-46;
 RESULT 813
 ID ADL09103 standard; DNA; 148567 BP.
 DE Human protein kinase, genomic DNA.
 Query Match 21.9%; Score 199; DB 12; Length 148567;
 Best Local Similarity 79.3%; Pred. No. 8.1e-46;
 RESULT 814
 ID ACF62711 standard; DNA; 189013 BP.
 DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:669.
 PN WO2003013534-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDIATROS BIOTECHNOLOGIE AG.
 Query Match 21.9%; Score 199; DB 8; Length 189013;
 Best Local Similarity 82.6%; Pred. No. 8.9e-46;
 RESULT 815
 ID AUB20836 standard; DNA; 189013 BP.
 DE MRPI based cancer related nucleic acid SEQ ID NO:669.
 PN WO2003013535-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDIATROS BIOTECHNOLOGIE AG.
 Query Match 21.9%; Score 199; DB 8; Length 189013;
 Best Local Similarity 82.6%; Pred. No. 8.9e-46;
 RESULT 816
 ID ADB87945 standard; DNA; 189013 BP.
 DE Human uterine gene sequence SEQ ID NO:669.
 PN WO2003013535-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDIATROS BIOTECHNOLOGIE AG.
 Query Match 21.9%; Score 199; DB 10; Length 189013;
 Best Local Similarity 82.6%; Pred. No. 8.9e-46;
 RESULT 817
 ID ADB96928 standard; DNA; 189013 BP.
 DE Human MRPI related DNA sequence SEQ ID NO:669.
 PN WO2003013537-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDIATROS BIOTECHNOLOGIE AG.
 Query Match 21.9%; Score 199; DB 10; Length 189013;
 Best Local Similarity 82.6%; Pred. No. 8.9e-46;
 RESULT 818
 ID ADB92119 standard; DNA; 189013 BP.
 DE Human MRPI related DNA sequence SEQ ID NO:669.
 PN WO2003013535-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDIATROS BIOTECHNOLOGIE AG.
 Query Match 21.9%; Score 199; DB 10; Length 189013;
 Best Local Similarity 82.6%; Pred. No. 8.9e-46;
 RESULT 819
 ID ACM44170 standard; DNA; 196686 BP.
 DE Human genomic sequence hCG39530.
 PN WO2003073826-A2.
 PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY. 21.9%; Score 199; DB 11; Length 196686;
 Best Local Similarity 81.3%; Pred. No. 9.1e-46;
 RESULT 820
 ID ADU8916 standard; DNA; 349989 BP.
 DR Human GPCR gene SEQ ID NO:1359.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAD-) NAT INST ADVANCED SCI & TECHNOLOGY INCUBATIO.
 (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 21.9%; Score 199; DB 10; Length 349989;
 Best Local Similarity 78.5%; Pred. No. 1.1e-45;
 RESULT 821
 ID ABN62834 standard; cDNA; 402 BP.
 DR Human cancer related polynucleotide SEQ ID NO 2801.
 PN WO20014500-A2.
 PD 21-FEB-2002.
 PA (CHIR) CHIRON CORP.
 (HYSE-) HYSEQ INC.
 Query Match 21.9%; Score 198.8; DB 6; Length 402;
 Best Local Similarity 79.6%; Pred. No. 9.5e-47;
 RESULT 822
 ID AAK7637 standard; DNA; 2173 BP.
 DR Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30449.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.8; DB 4; Length 2173;
 Best Local Similarity 75.2%; Pred. No. 1.8e-46;
 RESULT 823
 ID AAK16224 standard; cDNA; 2591 BP.
 DR Human cDNA sequence SEQ ID NO:15042.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 21.9%; Score 198.8; DB 4; Length 2591;
 Best Local Similarity 81.8%; Pred. No. 2e-46;
 RESULT 824
 ID ADL22885 standard; DNA; 2591 BP.
 DR Human MP2153 coding sequence SEQ ID NO: 5.
 PN WO2004015009-A2.
 PD 19-FEB-2004.
 PA (EXEL-) EXELIXIS INC.
 Query Match 21.9%; Score 198.8; DB 12; Length 2591;
 Best Local Similarity 81.8%; Pred. No. 2e-46;
 RESULT 825
 ID ADR1082 standard; DNA; 2591 BP.
 DR Human NF-kappaB pathway-associated gene seqID83.
 PN WO2004055577-A2.
 PD 05-AUG-2004.
 PA (IBRM) BRISTOL-MYERS SQUIBB CO.
 Query Match 21.9%; Score 198.8; DB 13; Length 2591;
 Best Local Similarity 81.8%; Pred. No. 2e-46;
 RESULT 826
 ID ADR0024 standard; cDNA; 3385 BP.
 DR Full length human cDNA useful for treating neurological disease Seq 1530.
 PN EP1447413-A2.
 PD 18-AUG-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 21.9%; Score 198.8; DB 13; Length 3385;
 Best Local Similarity 85.9%; Pred. No. 2.2e-46;
 RESULT 827
 ID ACN37218 standard; DNA; 20001 BP.
 DR Human periodontal disease related gene PRGD2 SEQ ID NO:128.
 PN WO2004042054-A1.
 PD 21-MAY-2004.
 PA (HUBT-) HUBIT GENOMIX INC.
 (KAMO-) KAMOI K.
 Query Match 21.9%; Score 198.8; DB 13; Length 20001;
 Best Local Similarity 83.0%; Pred. No. 4.3e-46;
 RESULT 828
 ID AAK81266 standard; DNA; 21458 BP.
 DR Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36078.

PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.8; DB 4; Length 21458;
 Best Local Similarity 82.1%; Pred. No. 4.4e-46;
 RESULT 829
 ID AAL0612 standard; DNA; 21458 BP.
 DR Human reproductive system related antigen DNA SEQ ID NO: 8810.
 PN WO20015320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.8; DB 4; Length 21458;
 Best Local Similarity 82.1%; Pred. No. 4.4e-46;
 RESULT 830
 ID ABL9687 standard; DNA; 21458 BP.
 DR Human testicular antigen encoding DNA fragment SEQ ID NO: 3339.
 PN WO20015317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.8; DB 4; Length 21458;
 Best Local Similarity 82.1%; Pred. No. 4.4e-46;
 RESULT 831
 ID ABK42270 standard; DNA; 21470 BP.
 DR Genomic sequence #169 encoding novel human connective tissue polypeptide.
 PN WO20015333-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.8; DB 4; Length 21470;
 Best Local Similarity 83.0%; Pred. No. 4.4e-46;
 RESULT 832
 ID ADB60426 standard; DNA; 21470 BP.
 DR Connective tissue related genomic DNA #169.
 PN US2003054375-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.8; DB 9; Length 21470;
 Best Local Similarity 83.0%; Pred. No. 4.4e-46;
 RESULT 833
 ID ADA2702 standard; DNA; 21666 BP.
 DR Human Nuprl carcinoma associated gene, SEQ ID NO:1220.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.9%; Score 198.8; DB 9; Length 21666;
 Best Local Similarity 84.9%; Pred. No. 4.4e-46;
 RESULT 834
 ID ADB7440 standard; DNA; 21666 BP.
 DR Human CA gene.
 PN WO200305593-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.9%; Score 198.8; DB 10; Length 21666;
 Best Local Similarity 84.9%; Pred. No. 4.4e-46;
 RESULT 835
 ID ADB95950 standard; DNA; 21666 BP.
 DR Human HCG745228 gene genomic DNA sequence.
 PN WO200303984-A2.
 PD 15-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.9%; Score 198.8; DB 10; Length 21666;
 Best Local Similarity 84.9%; Pred. No. 4.4e-46;
 RESULT 836
 ID ADK4307 standard; DNA; 23469 BP.
 DR Human HNFalpha gene SEQ ID NO:27.
 PN WO2003016013-A2.
 PD 26-FEB-2004.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 Query Match 21.9%; Score 198.8; DB 12; Length 23469;
 Best Local Similarity 77.3%; Pred. No. 4.6e-46;
 RESULT 837
 ID ACN3724 standard; DNA; 25382 BP.
 DR Human periodontal disease gene IL4R SEQ ID NO:154.
 PN WO200303984-A2.

Best Local Similarity 82.1%; Pred. No. 4.7e-46;
 RESULT 838
 ID AAF57718 standard; DNA; 28690 BP.
 DB Human IL4Ralpha gene.
 PN WO200104270-A1.
 PD 18-JAN-2001.
 PA (GENA-) GENNAISANCE PHARM INC.
 Query Match 21.9%; Score 198.8; DB 5; Length 28690;
 Best Local Similarity 82.1%; Pred. No. 4.9e-46;
 RESULT 839
 ID ADN3674 standard; DNA; 4047 BP.
 DE Human autoimmune disease-related genomic DNA sequence - SEQ ID NO:1688.
 PA (APPL-) APIPLERA CORP.
 Best Local Similarity 79.7%; Pred. No. 5.7e-46;
 RESULT 840
 ID AAK65631 standard; DNA; 41159 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20443.
 PN WO20015182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.8; DB 13; Length 40947;
 Best Local Similarity 81.2%; Pred. No. 5.7e-46;
 RESULT 841
 ID ADN3602 standard; DNA; 43950 BP.
 DE Human kinase genomic DNA.
 PN WO2004058144-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.9%; Score 198.8; DB 6; Length 43950;
 Best Local Similarity 81.2%; Pred. No. 5.8e-46;
 RESULT 842
 ID ABD33486 standard; DNA; 51289 BP.
 DE Human cancer-associated (CA) gene HD07-094.
 PN WO2004058144-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.9%; Score 198.8; DB 13; Length 51289;
 Best Local Similarity 86.2%; Pred. No. 6.2e-46;
 RESULT 843
 ID ABD33339 standard; DNA; 62658 BP.
 DE Human cancer-associated (CA) gene HD07-061.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.9%; Score 198.8; DB 13; Length 62658;
 Best Local Similarity 81.2%; Pred. No. 6.7e-46;
 RESULT 844
 ID ACM44522 standard; DNA; 70779 BP.
 DE Human genomic sequence hCG17357.
 PN WO200307326-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.9%; Score 198.8; DB 11; Length 70779;
 Best Local Similarity 82.1%; Pred. No. 7.e-46;
 RESULT 845
 ID ABH64158 standard; DNA; 84539 BP.
 DE Stomach cancer related gene sequence SEQ ID NO:2495.
 PN WO200104629-A2.
 PD 15-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 21.9%; Score 198.8; DB 6; Length 84539;
 Best Local Similarity 75.6%; Pred. No. 7.5e-46;
 RESULT 846
 ID ADU13479 standard; DNA; 84539 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #11.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYBE GENOMICS INC.
 Query Match 21.9%; Score 198.8; DB 10; Length 84539;
 Best Local Similarity 75.6%; Pred. No. 7.5e-46;
 RESULT 847
 ID ADM29048 standard; DNA; 130020 BP.
 DE Human interleukin 4 receptor (IL4R) genomic DNA SEQ ID NO:88.

PN EP1405921-A1.
 PD 07-APR-2004.
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 Query Match 21.9%; Score 198.8; DB 12; Length 130020;
 Best Local Similarity 82.1%; Pred. No. 8.8e-46;
 RESULT 848
 ID ACN44070 standard; DNA; 344548 BP.
 DE Human genomic sequence hCG36954.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.9%; Score 198.8; DB 11; Length 344548;
 Best Local Similarity 83.3%; Pred. No. 1.3e-45;
 RESULT 849
 ID ADQ97146 standard; DNA; 348101 BP.
 DE Human cancer-associated sequence HD08-007, SEQ ID NO:122.
 PN WO2004050304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.9%; Score 198.8; DB 12; Length 348101;
 Best Local Similarity 82.1%; Pred. No. 1.3e-45;
 RESULT 850
 ID AAS62592 standard; cDNA; 1191 BP.
 DE cDNA Sequence #379 encoding novel human secreted protein.
 PN WO20017291-A2.
 PD 18-OCT-2001.
 PA (GEMY) GENETICS INST INC.
 Query Match 21.9%; Score 198.6; DB 6; Length 1191;
 Best Local Similarity 85.4%; Pred. No. 1.7e-46;
 RESULT 851
 ID AA158575 standard; cDNA; 1946 BP.
 DE Human Pyrimidoleotide SEQ ID NO 778.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 21.9%; Score 198.6; DB 4; Length 1946;
 Best Local Similarity 82.8%; Pred. No. 2e-46;
 RESULT 852
 ID ADQ98192 standard; cDNA; 1946 BP.
 DE DNA encoding human GPCR-like protein seqid 462.
 PN US6569652-B1.
 PD 27-MAY-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 21.9%; Score 198.6; DB 5; Length 1946;
 Best Local Similarity 82.8%; Pred. No. 2e-46;
 RESULT 853
 ID AB48552 standard; cDNA; 1946 BP.
 DE Novel human cDNA SEQ ID NO 462.
 PN US2003104529-A1.
 PD 05-JUN-2003.
 PA (ZHOU/) ZHOU P.
 PA (TANG/) TANG Y. T.
 PA (LIUC/) LIU C.
 PA (ASUN/) ASUNDI V.
 PA (DRMA/) DRMANAC R T.
 Query Match 21.9%; Score 198.6; DB 9; Length 1946;
 Best Local Similarity 82.8%; Pred. No. 2e-46;
 RESULT 854
 ID AAK63412 standard; DNA; 4156 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38224.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.6; DB 4; Length 4156;
 Best Local Similarity 80.3%; Pred. No. 2.7e-46;
 RESULT 855
 ID AAK68677 standard; DNA; 4963 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23479.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.6; DB 4; Length 4963;

Best Local Similarity 80.3%; Pred. No. 2.9e-46;
 RESULT 855
 ID AAL36538 Standard; DNA; 4963 BP.
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 2903.
 PN WO200153567-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.6; DB 4; Length 4963;
 Best Local Similarity 80.3%; Pred. No. 2.9e-46;
 RESULT 857
 ID ABX5526 standard; cDNA; 4963 BP.
 DE cDNA encoding novel human musculoskeletal system antigen #1870.
 PN US2002147140-A1.
 PD 10-OCT-2002.
 ID ADJ3276 standard; DNA; 4963 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2903.
 PN US2004009488-A1.
 PD 15-JUN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.6; DB 8; Length 4963;
 Best Local Similarity 80.3%; Pred. No. 2.9e-46;
 RESULT 858
 ID ADP0579 standard; DNA; 5840 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30489.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.6; DB 12; Length 15297;
 Best Local Similarity 80.8%; Pred. No. 4.4e-46;
 RESULT 860
 ID AAK7567 standard; DNA; 16424 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30489.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.6; DB 4; Length 16424;
 Best Local Similarity 82.8%; Pred. No. 4.5e-46;
 RESULT 861
 ID ADP0579 standard; cDNA; 5840 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 85.
 PN EP147413-A2.
 PD 18-AUG-2004.
 PA (REAS-) RESS ASSOC BIOTECHNOLOGY.
 Query Match 21.9%; Score 198.6; DB 13; Length 5840;
 Best Local Similarity 82.8%; Pred. No. 3e-46;
 RESULT 860
 ID AAS26766 standard; DNA; 6096 BP.
 DE Human genomic DNA encoding partial novel secreted protein, Seq ID 1740.
 PN WO200155322-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.6; DB 4; Length 6096;
 Best Local Similarity 77.7%; Pred. No. 3.1e-46;
 RESULT 861
 ID ABX74115 standard; DNA; 6096 BP.
 DE Human novel polynucleotide #943.
 PN US2002132153-A1.
 PD 19-SEP-2002.
 PA (ROSE-) ROSEN C A.
 PA (RUBE-) RUBEN S M.
 PA (BARA-) BARASH S C.
 Query Match 21.9%; Score 198.6; DB 8; Length 6096;
 Best Local Similarity 77.7%; Pred. No. 3.1e-46;
 RESULT 862
 ID ABK6351 standard; cDNA; 12263 BP.
 DE Human cDNA differentially expressed in granulocytic cells #1085.
 PN WO200228939-A2.
 PD 11-APR-2002.
 PA (GENB-) GENB LOGIC INC.
 Query Match 21.9%; Score 198.6; DB 6; Length 12263;
 Best Local Similarity 80.8%; Pred. No. 4.1e-46;
 RESULT 863
 ID ABA94501 standard; DNA; 15297 BP.
 DE Human proto-oncogene tyrosine kinase genomic DNA sequence.
 PN US6340584-B1.
 PD 22-JAN-2002.
 PA (PEKR-) PE CORP NY.
 Query Match 21.9%; Score 198.6; DB 6; Length 15297;
 Best Local Similarity 80.8%; Pred. No. 4.4e-46;
 RESULT 864
 ID ABV75414 standard; DNA; 15297 BP.
 DE Human kinase genomic DNA sequence.
 PN WO2002277191-A2.

PD 03-OCT-2002.
 PA (PEKE-) PE CORP NY.
 Query Match 21.9%; Score 198.6; DB 8; Length 15297;
 Best Local Similarity 80.8%; Pred. No. 4.4e-46;
 RESULT 865
 ID ADM2582 Standard; cDNA; 15297 BP.
 DE Human proto-oncogene tyrosine kinase DNA.
 PN US2004063130-A1.
 PD 01-APR-2004.
 PA (APPL-) APPLEA CORP.
 Query Match 21.9%; Score 198.6; DB 12; Length 15297;
 Best Local Similarity 80.8%; Pred. No. 4.4e-46;
 RESULT 866
 ID AAK7567 standard; DNA; 16424 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30489.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.6; DB 4; Length 16424;
 Best Local Similarity 82.8%; Pred. No. 4.5e-46;
 RESULT 867
 ID AAK63448 standard; DNA; 16424 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23260.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.6; DB 4; Length 16424;
 Best Local Similarity 82.8%; Pred. No. 4.5e-46;
 RESULT 868
 ID ABA08132 standard; DNA; 32152 BP.
 DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 927.
 PN WO200155325-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.6; DB 4; Length 32152;
 Best Local Similarity 74.8%; Pred. No. 5.9e-46;
 RESULT 869
 ID ADP7184 standard; DNA; 35192 BP.
 DE Human ADAM19 gene fragment #4.
 PN WO2003031594-A2.
 PD 17-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 21.9%; Score 198.6; DB 11; Length 35192;
 Best Local Similarity 82.8%; Pred. No. 6.1e-46;
 RESULT 870
 ID ADQ97084 standard; DNA; 38690 BP.
 DE Human cancer associated sequence HD10-004, SEQ ID 60.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.9%; Score 198.6; DB 12; Length 38690;
 Best Local Similarity 82.8%; Pred. No. 6.3e-46;
 RESULT 871
 ID AAK76219 standard; DNA; 47090 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33031.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.6; DB 4; Length 47090;
 Best Local Similarity 79.2%; Pred. No. 6.8e-46;
 RESULT 872
 ID AAK6725 standard; DNA; 47090 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23537.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.6; DB 4; Length 47090;
 Best Local Similarity 79.2%; Pred. No. 6.8e-46;
 RESULT 873
 ID ABQ7689 standard; DNA; 53225 BP.
 DE Human G-protein coupled receptor DNA SEQ ID 3.
 PN US2002142951-A1.
 PD 03-OCT-2002.

PA (WEBB-) WEBSTER M.
 PA (BEAS-) BEASLEY B M.
 PA (KETC-) KETCHUM K A.
 PA (DPRV-) DI FRANCESCO V.
 Query Match 21.9%; Score 198.6; DB 10; Length 53226;
 Best Local Similarity 82.8%; Pred. No. 7.1e-46;
 RESULT 874
 ID ADJ84182 standard; DNA; 76698 BP.
 DE Human C-rat genomic DNA which is a target for antisense therapy.
 PN WO2004003134-A2.
 PD 08-JAN-2004.

PA (ISIS-) ISIS PHARM INC. 21.9%; Score 198.6; DB 12; Length 76698;
 Best Local Similarity 82.8%; Pred. No. 8.2e-46;
 RESULT 875
 ID AB08164 standard; cDNA; 86080 BP.
 DE Human osteoblast differentiation related cDNA SEQ ID NO 71.
 PN WO20025030-A2.
 PD 27-JUN-2002.

PA (GENE-) GENE LOGIC INC.
 Query Match 21.9%; Score 198.6; DB 6; Length 86080;
 Best Local Similarity 82.7%; Pred. No. 8.6e-46;
 RESULT 876
 ID ABK83561 standard; cDNA; 86080 BP.
 DE Human CDNA differentially expressed in granulocytic cells #132.
 PN WO200228999-A2.

PA (PROT-) PROCTER & GAMBLE CO.
 Query Match 21.9%; Score 198.6; DB 6; Length 86080;
 Best Local Similarity 82.7%; Pred. No. 8.6e-46;
 RESULT 877
 ID ADP71054 standard; DNA; 86080 BP.
 DE Human protective protein for beta-galactosidase gene SEQ ID NO:58.
 PN WO200361565-A2.
 PD 11-APR-2002.

PA (GENE-) GENE LOGIC INC.
 Query Match 21.9%; Score 198.6; DB 6; Length 86080;
 Best Local Similarity 82.7%; Pred. No. 8.6e-46;
 RESULT 878
 ID ADQ18878 standard; DNA; 86080 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1697.
 PN WO2004048938-A2.

PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 21.9%; Score 198.6; DB 12; Length 86080;
 Best Local Similarity 82.7%; Pred. No. 8.6e-46;
 RESULT 879
 ID ADL13497 standard; DNA; 91823 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #29.
 PN WO2003054166-A2.
 PD 03-JUL-2003.

PA (INCY-) INCYTE GENOMICS INC.
 Query Match 21.9%; Score 198.6; DB 10; Length 91823;
 Best Local Similarity 82.7%; Pred. No. 8.8e-46;
 RESULT 880
 ID ACM44930 standard; DNA; 106378 BP.
 DE Human genomic Sequence hCG1742422.
 PN WO2003073826-A2.
 PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.9%; Score 198.6; DB 11; Length 106378;
 Best Local Similarity 80.3%; Pred. No. 9.3e-46;
 RESULT 881
 ID ADG32260 standard; DNA; 106707 BP.
 DE Human chromosome 20 region containing type 2 diabetes mellitus genes.
 PN WO2004039954-A2.
 PD 13-MAY-2004.

PA (JOSL-) JOSLIN DIABETES CENT INC.
 Query Match 21.9%; Score 198.6; DB 12; Length 106707;
 Best Local Similarity 82.8%; Pred. No. 9.3e-46;
 RESULT 882

Query Match 21.9%; Score 198.6; DB 13; Length 118466;
 Best Local Similarity 82.8%; Pred. No. 9.7e-46;
 RESULT 883
 ID ABD32861 standard; DNA; 118466 BP.
 DE Human cancer-associated genomic DNA HD17-042.
 PN WO2004074320-A2.
 PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.9%; Score 198.6; DB 12; Length 121160;
 Best Local Similarity 84.3%; Pred. No. 9.8e-46;
 RESULT 884
 ID ABG7070 standard; DNA; 121160 BP.
 DE Human cancer associated Sequence HD11-015, SEQ ID 847.
 PN WO2004060304-A2.
 PD 22-JUL-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.9%; Score 198.6; DB 12; Length 122748;
 Best Local Similarity 84.3%; Pred. No. 9.8e-46;
 RESULT 885
 ID ABT10719 standard; cDNA; 122748 BP.
 DE Human breast cancer associated coding sequence SEQ ID NO: 853.
 PN WO200229271-A2.

PA (GENE-) GENE LOGIC INC. 21.9%; Score 198.6; DB 6; Length 145831;
 Best Local Similarity 80.3%; Pred. No. 9.9e-46;
 RESULT 886
 ID ABU69213 standard; DNA; 145831 BP.
 DE Prostate cancer related gene sequence SEQ ID NO:7550.
 PN WO200194629-A2.
 PD 13-DEC-2001.

PA (AVAL-) AVALON PHARM.
 Query Match 21.9%; Score 198.6; DB 6; Length 145831;
 Best Local Similarity 79.2%; Pred. No. 1.1e-45;
 RESULT 887
 ID ABU66806 standard; DNA; 145831 BP.
 DE Lung cancer related gene sequence SEQ ID NO:5143.
 PN WO200194629-A2.
 PD 13-DEC-2001.

PA (AVAL-) AVALON PHARM.
 Query Match 21.9%; Score 198.6; DB 6; Length 145831;
 Best Local Similarity 79.2%; Pred. No. 1.1e-45;
 RESULT 888
 ID ABU68588 standard; DNA; 145831 BP.
 DE Kidney cancer related gene sequence SEQ ID NO:6925.
 DE Lung cancer related gene sequence SEQ ID NO:6925.
 PN WO200194629-A2.
 PD 13-DEC-2001.

PA (AVAL-) AVALON PHARM.
 Query Match 21.9%; Score 198.6; DB 6; Length 145831;
 Best Local Similarity 79.2%; Pred. No. 1.1e-45;
 RESULT 889
 ID ABU62309 standard; DNA; 145831 BP.
 DE Colon adenocarcinoma related gene sequence SEQ ID NO:6465.
 PN WO200194629-A2.
 PD 13-DEC-2001.

PA (AVAL-) AVALON PHARM.
 Query Match 21.9%; Score 198.6; DB 6; Length 145831;
 Best Local Similarity 79.2%; Pred. No. 1.1e-45;
 RESULT 890
 ID ABU62309 standard; DNA; 145831 BP.
 DE Colon adenocarcinoma related gene sequence SEQ ID NO:6465.
 PN WO200194629-A2.
 PD 13-DEC-2001.

PA (AVAL-) AVALON PHARM.
 Query Match 21.9%; Score 198.6; DB 6; Length 145831;
 Best Local Similarity 79.2%; Pred. No. 1.1e-45;
 RESULT 891
 ID ABT1049 standard; cDNA; 145831 BP.
 DE Human breast cancer associated coding sequence SEQ ID NO: 283.
 PN WO200252271-A2.
 PD 01-AUG-2002.

PA (GENE-) GENE LOGIC INC.
 Query Match 21.9%; Score 198.6; DB 6; Length 145831;
 Best Local Similarity 79.2%; Pred. No. 1.1e-45;
 RESULT 892
 ID ABG92378 standard; DNA; 700 BP.
 DE Human inflammatory bowel disease related gene fragment IGR1078A.
 PN WO200142511-A2.

PD 14-JUN-2001.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
Query Match
Best Local Similarity 84.8%; Pred. No. 1.5e-46;
RESULT 893
ID ABK42296 standard; DNA; 1672 BP.
DE Genomic sequence #195 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.4; DB 4; Length 1672;
Best Local Similarity 81.0%; Pred. No. 2.2e-46;
RESULT 894
ID ADB60452 standard; DNA; 1672 BP.
DE Connective tissue related genomic DNA #195.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.4; DB 9; Length 1672;
Best Local Similarity 81.0%; Pred. No. 2.2e-46;
RESULT 895
ID ADM02728 standard; cDNA; 2549 BP.
DE Human cDNA of the invention SEQ ID NO:1413.
PN EP134046-A1.
PD 24-SEP-2003.
PA (REAS-) REBS ASSOC BIOTECHNOLOGY
Query Match 21.9%; Score 198.4; DB 11; Length 2549;
Best Local Similarity 78.8%; Pred. No. 2.5e-46;
RESULT 896
ID ABA21351 standard; DNA; 3843 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13682.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.4; DB 5; Length 3843;
Best Local Similarity 77.2%; Pred. No. 3e-46;
RESULT 897
ID AAT75298 standard; DNA; 7705 BP.
DE Nucleotide sequence encoding human RAD50 3' end.
PN WO9722784-A2.
PD 19-JUN-1997.
PA (GENE-) GENBLABS TECHNOLOGIES INC.
Query Match 21.9%; Score 198.4; DB 2; Length 7705;
Best Local Similarity 84.8%; Pred. No. 3.9e-46;
RESULT 898
ID ABK8618 standard; DNA; 13919 BP.
DE DNA encoding AIP-1/FLASH promoter.
PN WO200255691-A1.
PD 18-JUL-2002.
PA (NIPK) NIPPON KAYAKU KK.
Query Match 21.9%; Score 198.4; DB 6; Length 13919;
Best Local Similarity 78.8%; Pred. No. 4.9e-46;
RESULT 899
ID ABK86221 standard; RNA; 13919 BP.
DE AIP-1/FLASH promoter related RNA sequence.
PN WO200255691-A1.
PD 18-JUL-2002.
PA (NIPK) NIPPON KAYAKU KK.
Query Match 21.9%; Score 198.4; DB 6; Length 13919;
Best Local Similarity 78.8%; Pred. No. 4.9e-46;
RESULT 900
ID ABK86220 standard; DNA; 13919 BP.
DE AIP-1/FLASH promoter related DNA sequence #2.
PN WO200255691-A1.
PD 18-JUL-2002.
PA (NIPK) NIPPON KAYAKU KK.
Query Match 21.9%; Score 198.4; DB 6; Length 13919;
Best Local Similarity 78.8%; Pred. No. 4.9e-46;
RESULT 901
ID ABK86229 standard; DNA; 21404 BP.
DE AIP-1/FLASH promoter related DNA sequence #3.
PN WO200255691-A1.

PD 18-JUL-2002.
PA (NIPK) NIPPON KAYAKU KK.
Query Match 21.9%; Score 198.4; DB 6; Length 21404;
Best Local Similarity 78.8%; Pred. No. 5.7e-46;
RESULT 902
ID ADP6594 standard; DNA; 22405 BP.
DE Human cancer associated gene genomic sequence SEQ ID NO:40.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SACRES DISCOVERY INC.
Query Match 21.9%; Score 198.4; DB 13; Length 22405;
Best Local Similarity 82.2%; Pred. No. 5.8e-46;
RESULT 903
ID ADS31465 standard; DNA; 25322 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1679.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 21.9%; Score 198.4; DB 13; Length 25322;
Best Local Similarity 78.8%; Pred. No. 6.1e-46;
RESULT 904
ID ADQ91719 standard; DNA; 29360 BP.
DE Human cancer associated sequence HD08-012, SEQ ID 165.
PN WO2004050304-A2.
PD 22-JUL-2004.
PA (SAGR-) SACRES DISCOVERY INC.
Query Match 21.9%; Score 198.4; DB 12; Length 29360;
Best Local Similarity 79.9%; Pred. No. 6.5e-46;
RESULT 905
ID AAK89230 standard; DNA; 30110 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2806.
PN WO20015314-A2.
PD 02-AUG-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.4; DB 4; Length 30110;
Best Local Similarity 78.4%; Pred. No. 6.5e-46;
RESULT 906
ID ADS36492 standard; DNA; 34059 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1706.
PN WO2004083403-A2.
DE Human WKL-1 genomic DNA.
PN EP1209229-A1.
PD 29-MAY-2002.
PA (LESC/) LIESCH K.
Query Match 21.9%; Score 198.4; DB 13; Length 34059;
Best Local Similarity 78.8%; Pred. No. 6.9e-46;
RESULT 907
ID AAB31198 standard; DNA; 34634 BP.
DE Human WKL-1 genomic DNA.
PN EP1209229-A1.
PD 21-MAY-2004.
PA (HUBI-) HUBIT GENOMIX INC.
Query Match 21.9%; Score 198.4; DB 6; Length 34634;
Best Local Similarity 79.9%; Pred. No. 6.9e-46;
RESULT 908
ID ACN323 standard; DNA; 48753 BP.
DE Human periodontal disease related gene HSPG2 SEQ ID NO:148.
PN WO2004042054-A1.
PD 21-MAY-2004.
PA (KAMO-) KAMO K.
Query Match 21.9%; Score 198.4; DB 13; Length 48753;
Best Local Similarity 84.8%; Pred. No. 7.9e-46;
RESULT 909
ID ACN4516 standard; DNA; 87687 BP.
DE Human genomic Sequence HG337872.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 198.4; DB 11; Length 87687;
Best Local Similarity 83.0%; Pred. No. 9.9e-46;
RESULT 910
ID ADP1458 standard; DNA; 87869 BP.
DE Renal cell carcinoma differentially expressed gene #194.

- PN WO2004048933-A2.
 PD 03-OCT-2002.
 PA (YANCI) YAN C.
 PA (KETCHUM) KETCHUM K A.
 PA (KETC/) KETCHUM K A.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E M.
 PA (TREP/) BURCZYNSKI M E.
 PA (DORN/) DORNER A.
 PA (STOV/) STOVER J A.
 PA (SAGR-) SAGRE DISCOVERY.
 Best Local Similarity 21.9%; Score 198.4; DB 12; Length 87869;
 RESULT 911
 ID ACM45042 standard; DNA; 95835 BP.
 DE Human genomic sequence hCG37223.
 PN WO2003073026-A2.
 PD 12-SEP-2003.
 ID ADE43582 standard; DNA; 128034 BP.
 DE Polymorphic human IDS genomic sequence, SEQ ID 187.
 PN WO2003054143-A2.
 PD 03-JUL-2003.
 ID (NEUR-) NEUROGENETICS INC.
 PA (GEHO) GEN HOSPITAL CORP.
 Query Match 21.9%; Score 198.4; DB 10; Length 95835;
 Best Local Similarity 79.6%; Pred. No. 1.e-45;
 RESULT 912
 ID ADHS4060 standard; DNA; 128034 BP.
 DE Human IDE gene variant DNA sequence SeqID187.
 PN US2003224360-A1.
 PD 04-DEC-2003.
 PA (GENO) GEN HOSPITAL CORP.
 Best Local Similarity 79.6%; Pred. No. 1.e-45;
 RESULT 913
 ID ABK8373 standard; cDNA; 130263 BP.
 DE Human cDNA differentially expressed in granulocytic cells #144.
 PN WO20032899-A2.
 PD 11-APR-2002.
 PA (GENE-) GENB LOGIC INC.
 Best Local Similarity 81.0%; Pred. No. 1.2e-45;
 RESULT 914
 ID ABL1336 standard; DNA; 143899 BP.
 DE Genomic sequence encoding a human Ngr2 protein.
 PN WO200229059-A2.
 PD 11-APR-2002.
 PA (UYA) UNIV YALE.
 PA (BIOJ) BIOCEN INC.
 Query Match 21.9%; Score 198.4; DB 6; Length 130263;
 Best Local Similarity 81.0%; Pred. No. 1.2e-45;
 RESULT 915
 ID ABL1336 standard; DNA; 143899 BP.
 DE Genomic sequence encoding a human Ngr2 protein.
 PN WO200229059-A2.
 PD 11-APR-2002.
 PA (UYA) UNIV YALE.
 PA (BIOJ) BIOCEN INC.
 Query Match 21.9%; Score 198.4; DB 6; Length 143899;
 Best Local Similarity 81.0%; Pred. No. 1.2e-45;
 RESULT 916
 ID ABL68122 standard; DNA; 174424 BP.
 DE Ovary cancer related gene Sequence SEQ ID NO:6459.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 21.9%; Score 198.4; DB 6; Length 174424;
 Best Local Similarity 84.8%; Pred. No. 1.3e-45;
 RESULT 917
 ID AD019573 standard; DNA; 181343 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2392.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 21.9%; Score 198.4; DB 12; length 181343;
 Best Local Similarity 84.8%; Pred. No. 1.3e-45;
 RESULT 918
 ID ABX16034 standard; DNA; 203654 BP.
 DE Human gene encoding calcium channel transporter family member.
 PN US2002142938-A1.
- PN WO2004048933-A2.
 PD 03-OCT-2002.
 PA (YANCI) YAN C.
 PA (KETCHUM) KETCHUM K A.
 PA (KETC/) KETCHUM K A.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E M.
 Query Match 21.9%; Score 198.4; DB 10; length 203654;
 Best Local Similarity 84.8%; Pred. No. 1.4e-45;
 RESULT 919
 ID ADL1471 standard; DNA; 214520 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #3.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTB GENOMICS INC.
 Query Match 21.9%; Score 198.4; DB 10; Length 214520;
 Best Local Similarity 79.9%; Pred. No. 1.4e-45;
 RESULT 920
 ID AAIV57926 standard; DNA; 235033 BP.
 DE Hereditary haemochromatosis subregion from an unaffected individual.
 PN WO814466-A1.
 PD 09-APR-1998.
 PA (PROG-) PROGENITOR INC.
 Query Match 21.9%; Score 198.4; DB 2; Length 235033;
 Best Local Similarity 82.2%; Pred. No. 1.4e-45;
 RESULT 921
 ID AAK66647 standard; DNA; 598 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21459.
 PN WO20015182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.4; DB 4; Length 598;
 Best Local Similarity 81.0%; Pred. No. 1.7e-46;
 RESULT 922
 ID ADO15750 standard; DNA; 1714 BP.
 DE 4 synthesis-period of neuroblastoma related DNA, SEQ ID 12.
 PN WO200303975-A1.
 PD 13-MAY-2004.
 PA (HISM) HISAMITSU PHARM CO LTD.
 PA (CHIB-) CHIBA PREFECTURE.
 Query Match 21.9%; Score 198.2; DB 12; Length 1714;
 Best Local Similarity 80.5%; Pred. No. 2.5e-46;
 RESULT 923
 ID ADM02856 standard; cDNA; 2052 BP.
 DE Human cDNA of the invention SEQ ID NO:1541.
 PN EP1347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 21.9%; Score 198.2; DB 11; Length 2062;
 Best Local Similarity 72.7%; Pred. No. 2.7e-16;
 RESULT 924
 ID ABK34800 standard; cDNA; 2541 BP.
 DE Human cDNA for novel secreted protein, SEQ ID 569.
 PN WO200177290-A2.
 PD 18-OCT-2001.
 PA (GEM-) GENETICS INST INC.
 Query Match 21.9%; Score 198.2; DB 6; Length 2541;
 Best Local Similarity 82.9%; Pred. No. 2.9e-46;
 RESULT 925
 ID ABK70289 standard; cDNA; 4824 BP.
 DE Human lung cancer associated full length cDNA DSM-59.
 PN WO200224057-A2.
 PD 28-MAR-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 21.9%; Score 198.2; DB 6; Length 4824;
 Best Local Similarity 72.7%; Pred. No. 3.7e-46;
 RESULT 926
 ID ABK28814 standard; DNA; 4824 BP.
 DE Human chronic myelogenous leukaemia (CML) gene marker #82.
 PN US2003104426-A1.
 PD 05-JUN-2003.
 PA (LINS-) LINSLEY P S.
 PA (NAOM-) MAO M.
 PA (DAIH-) DAI H.
 PA (HEYY-) HE Y.

PA (RAD1-) RADICH J P.
 Query Match Similarity 21.9%; Score 198.2; DB 10; Length 4824;
 Best Local Similarity 72.7%; Pred. No. 3.7e-46;

RESULT 927
 ID ADR0591 standard; cDNA; 4865 BP.
 DE Human full-length human cDNA useful for treating neurological disease Seq 97.
 PN EP1447413-A2.
 PD 18-AUG-2004.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match Similarity 21.9%; Score 198.2; DB 13; Length 4865;
 Best Local Similarity 81.3%; Pred. No. 3.7e-46;

RESULT 928
 ID AS44656 standard; DNA; 4885 BP.
 DE Human full-length polynucleotide sequence #81.
 PN WO200164834-A2.

PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.
 Query Match Similarity 21.9%; Score 198.2; DB 4; Length 4885;
 Best Local Similarity 72.7%; Pred. No. 3.7e-46;

RESULT 929
 ID AAK80970 standard; DNA; 6159 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35782.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Similarity 21.9%; Score 198.2; DB 4; Length 6159;
 Best Local Similarity 80.8%; Pred. No. 4.1e-46;

RESULT 930
 ID AAD3327 standard; DNA; 15765 BP.
 DE Human NFKB1B gene, alternative version.

PN WO200212497-A2.

PD 14-FEB-2002.

PA (GENA-) GENNAISANCE PHARM INC.
 Query Match Similarity 21.9%; Score 198.2; DB 6; Length 15765;
 Best Local Similarity 79.2%; Pred. No. 5.8e-46;

RESULT 931
 ID AAD2179 standard; DNA; 15765 BP.
 DE Human NFKB1B gene.
 PN WO200212497-A2.

PD 14-FEB-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Similarity 21.9%; Score 198.2; DB 6; Length 15765;
 Best Local Similarity 79.2%; Pred. No. 5.8e-46;

RESULT 932
 ID AAK74096 standard; DNA; 21777 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28908.

PN WO200157782-A2.
 PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Similarity 21.9%; Score 198.2; DB 4; Length 21777;
 Best Local Similarity 80.5%; Pred. No. 6.6e-46;

RESULT 933
 ID AAS17764 standard; DNA; 24843 BP.
 DE Human Genomic DNA for CRBB1.

PN WO200185998-A1.
 PD 15-NOV-2001.

PA (GENA-) GENNAISANCE PHARM INC.
 Query Match Similarity 21.9%; Score 198.2; DB 6; Length 24843;
 Best Local Similarity 81.7%; Pred. No. 6.9e-46;

RESULT 934
 ID ADR7086 standard; DNA; 29328 BP.
 DE Human cancer associated gene genomic sequence SEQ ID NO:132.
 PN WO2004074321-A2.

PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match Similarity 21.9%; Score 198.2; DB 13; Length 29328;
 Best Local Similarity 77.4%; Pred. No. 7.4e-46;

RESULT 935
 ID ALU04340 standard; DNA; 32194 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 7028.

PN WO200155320-A2.
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match Similarity 21.9%; Score 198.2; DB 4; Length 32194;
 Best Local Similarity 82.9%; Pred. No. 7.7e-46;

RESULT 936
 ID ADS19371 standard; DNA; 37940 BP.
 DE Human PIP5K type II beta related DNA #1.
 PN US2003232777-A1.
 PD 18-DEC-2003.

PA (MARC-) MARCUSSON B G.
 PA (DOBI-) DOBIE K W.
 PA (FREI-) FREIER S M.
 Query Match Similarity 21.9%; Score 198.2; DB 13; Length 37940;
 Best Local Similarity 75.9%; Pred. No. 8.2e-46;

RESULT 937
 ID ADJ20093 standard; DNA; 38000 BP.
 DE Human PIPLC1-beta genomic DNA SeqID 11.
 PN US2003232775-A1.
 PD 18-DEC-2003.

PA (ISIS-) ISIS PHARM INC.
 Query Match Similarity 21.9%; Score 198.2; DB 12; Length 38000;
 Best Local Similarity 75.9%; Pred. No. 8.2e-46;

RESULT 938
 ID ACN45050 standard; DNA; 41966 BP.
 DE Human genomic sequence hCG39344.
 PN WO2003073826-A2.
 PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match Similarity 21.9%; Score 198.2; DB 11; Length 41965;
 Best Local Similarity 80.5%; Pred. No. 8.5e-46;

RESULT 939
 ID ADB16927 standard; DNA; 49806 BP.
 DE Human DYX11 DNA, chromosomal gene region nucleotides 50001-100000.
 PN WO2003068814-A1.
 PD 21-AUG-2003.

PA (LICIN-) LICENTIA LTD.
 Query Match Similarity 21.9%; Score 198.2; DB 9; Length 49806;
 Best Local Similarity 82.7%; Pred. No. 9.1e-46;

RESULT 940
 ID ABD32754 standard; DNA; 62124 BP.
 DE Human cancer-associated genomic DNA HD16-028.
 PN WO2004074320-A2.
 PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match Similarity 21.9%; Score 198.2; DB 13; Length 62124;
 Best Local Similarity 82.9%; Pred. No. 9.9e-46;

RESULT 941
 ID ADP05290 standard; DNA; 80928 BP.
 DE Human protein kinase C iota/lambda genomic sequence.
 PN WO2004041212-A2.
 PD 21-MAY-2004.

PA (SACK-) SACKTOR T C.
 PA (CRAR-) CRARY J F.
 PA (HERN-) HERNANDEZ A I.
 PA (MIRR-) MIRRA S.
 PA (SHAO-) SHAO C.
 Query Match Similarity 21.9%; Score 198.2; DB 12; Length 80928;
 Best Local Similarity 79.4%; Pred. No. 1.1e-45;

RESULT 942
 ID AAF4800 standard; DNA; 110000 BP.
 DE Nucleotide sequence of the human SPG4 gene.
 PN FR2798138-A1.
 PD 09-MAR-2001.

PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match Similarity 21.9%; Score 198.2; DB 5; Length 110000;
 Best Local Similarity 80.5%; Pred. No. 1.2e-45;

RESULT 943
 ID ACD13448 standard; DNA; 115756 BP.
 DE Human RNA encoding a p53 modifier; SEQ ID 68.
 PN WO200293122-A1.
 PD 12-DEC-2002.

PA (EXEL-) EXELIXIS INC.

Query Match 21.9%; Score 198.2; DB 8; Length 115756;
 Best Local Similarity 85.6%; Pred. No. 1.3e-45;

RESULT 945
 ID ADJ79962 standard; DNA; 123526 BP.
 DE Human glioma-associated oncogene-3 related DNA, SEQ ID NO 11.
 PN WO2003008549-A2.
 PD 30-JAN-2003.

Query Match 21.9%; Score 198.2; DB 10; Length 123526;
 Best Local Similarity 81.9%; Pred. No. 1.3e-45;

RESULT 946
 ID AAV57903 standard; DNA; 237326 BP.
 DE Hereditary haemochromatosis subregion from an HH affected individual.
 PN WO9814466-A1.

PD 09-APR-1998.

PA (PROG-) PROGENITOR INC.
 Query Match 21.9%; Score 198.2; DB 2; Length 237326;
 Best Local Similarity 82.9%; Pred. No. 1.7e-45;

RESULT 947
 ID ADQ59422 standard; DNA; 246940 BP.
 DE Human cancer-associated (Ca) gene sequence SEQ ID NO:58.
 PN WO200405208-A1.

PD 15-JUL-2004.

PA (SAGR-) SACCES DISCOVERY INC.
 Query Match 21.9%; Score 198.2; DB 12; Length 246940;
 Best Local Similarity 78.9%; Pred. No. 1.7e-45;

RESULT 948
 ID ADC87110 standard; DNA; 349999 BP.
 DE Human GPCR gene SEQ ID NO:1463.
 PN EP1270724-A2.

PD 02-JAN-2003.

PA (NADC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATO.
 Query Match 21.9%; Score 198.2; DB 10;
 Best Local Similarity 75.5%; Pred. No. 1.9e-45;

RESULT 949
 ID ADQ24208 standard; DNA; 1911 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7028.
 PN WO2004048938-A2.

PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 21.8%; Score 198; DB 12; Length 1911;
 Best Local Similarity 78.0%; Pred. No. 3e-46;

RESULT 950
 ID ADM01910 standard; cDNA; 2460 BP.
 DE Human cDNA of the invention SEQ ID NO:595.
 PN EP1347046-A1.

PD 24-SEP-2003.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 21.8%; Score 198; DB 11; Length 2460;
 Best Local Similarity 81.6%; Pred. No. 3.3e-46;

RESULT 951
 ID AAK68971 standard; DNA; 7770 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23783.
 PN WO200517182-A2.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 7770;
 Best Local Similarity 83.6%; Pred. No. 5.1e-46;

RESULT 952
 ID AAK6477 standard; DNA; 9409 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31289.
 PN WO200517182-A2.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 9409;
 Best Local Similarity 81.2%; Pred. No. 5.5e-46;

RESULT 953
 ID ADN34213 standard; DNA; 9432 BP.
 DE Human cytochrome P450 2D6 (CYP2D6) gene.
 PN WO00218638-A2.

PD 07-MAR-2002.

PA (GEMI-) GEMINI GENOMICS PLC.
 Query Match 21.8%; Score 198; DB 5; Length 11557;

Query Match 21.8%; Score 198; DB 6; Length 9432;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;

RESULT 954
 ID AC61301 standard; DNA; 9432 BP.
 DE Human cytochrome p450 gene CYP2D6, wild-type.
 PN EP1281755-A2.

PD 05-FEB-2003.

PA (PFIZ) PFIZER PROD INC.
 Query Match 21.8%; Score 198; DB 10; Length 9432;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;

RESULT 955
 ID ADP83400 standard; DNA; 9432 BP.
 DE Human CYP2D6 gene (wild-type).
 PN WO2003100091-A1.

PD 04-DEC-2003.

PA (BPIOD-) EPIAUDROS BIOTECHNOLOGIE AG.
 Query Match 21.8%; Score 198; DB 12; Length 9432;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;

RESULT 956
 ID ADJ70563 standard; DNA; 9432 BP.
 DE Human cytochrome P450 isoenzyme 2D6 genomic gene sequence SeqID1.
 PN WO200400970-A2.

PD 29-JAN-2004.

PA (BIOM-) BIOVENTURES INC.
 Query Match 21.8%; Score 198; DB 12; Length 9432;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;

RESULT 957
 ID ADM28891 standard; DNA; 9432 BP.
 DE Human wild-type CYP2D6 gene sequence.
 PN US2004072225-A1.

PD 15-APR-2004.

PA (DAWS-) DAWSON E.P.
 Query Match 21.8%; Score 198; DB 12; Length 9432;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;

RESULT 958
 ID ACG61502 standard; DNA; 9433 BP.
 DE Human cytochrome p450 gene CYP2D6, variant sequence.
 PN EP1281755-A2.

PD 05-FEB-2003.

PA (PFIZ) PFIZER PROD INC.
 Query Match 21.8%; Score 198; DB 10; Length 9433;
 Best Local Similarity 81.4%; Pred. No. 5.5e-16;

RESULT 959
 ID AAL06316 standard; DNA; 11557 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9064.
 PN WO20015320-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 11557;
 Best Local Similarity 82.6%; Pred. No. 5.9e-46;

RESULT 960
 ID AAL06315 standard; DNA; 11557 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9063.
 PN WO20015320-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 11557;
 Best Local Similarity 82.6%; Pred. No. 5.9e-46;

RESULT 961
 ID AAS32244 standard; DNA; 11557 BP.
 DE Human DNA repair and processing genomic DNA #30.
 PN WO20015204-A1.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 5; Length 11557;
 Best Local Similarity 82.6%; Pred. No. 5.9e-46;

RESULT 962
 ID AAS32243 standard; DNA; 11557 BP.
 DE Human DNA repair and processing genomic DNA #29.
 PN WO20015204-A1.

PD 02-AUG-2001.

Best Local Similarity 82.6%; Pred. No. 5.9e-46;
 RESULT 963
 ID ABS67547 Standard; DNA; 11557 BP.
 DE Novel human DNA repair protein, genomic sequence #30.
 PN US2002086353-A1.
 PD 04-JUL-2002.

PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.

Query Match 21.8%; Score 198; DB 6; Length 11557;
 Best Local Similarity 82.6%; Pred. No. 5.9e-46;
 ID ABS67546 Standard; DNA; 11557 BP.
 DE Novel human DNA repair protein, genomic sequence #29.
 PN US2002086353-A1.
 PD 04-JUL-2002.

PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.

Query Match 21.8%; Score 198; DB 6; Length 11557;
 Best Local Similarity 82.6%; Pred. No. 5.9e-46;
 RESULT 965
 ID AAK79132 Standard; DNA; 14379 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33944.
 PN WO200157182-A2.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 14379;
 Best Local Similarity 83.8%; Pred. No. 6.4e-46;
 RESULT 966
 ID AUS26724 Standard; DNA; 19472 BP.
 DE Human genomic DNA encoding partial novel secreted protein, Seq ID 1698.
 PN WO200155322-A2.
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 19472;
 Best Local Similarity 75.1%; Pred. No. 7.2e-46;
 RESULT 967
 ID ABX7073 Standard; DNA; 19472 BP.
 DE Human novel polynucleotide #901.
 PN US2002132253-A1.
 PD 19-SEP-2002.

PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.

Query Match 21.8%; Score 198; DB 8; Length 19472;
 Best Local Similarity 75.1%; Pred. No. 7.2e-46;
 RESULT 968
 ID AL03615 Standard; DNA; 32134 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 6303.
 PN WO200155320-A2.
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 32134;
 Best Local Similarity 82.4%; Pred. No. 8.7e-46;
 RESULT 969
 ID ABA07813 Standard; DNA; 32134 BP.
 DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 608.
 PN WO200155320-A2.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 32134;
 Best Local Similarity 82.4%; Pred. No. 8.7e-46;
 RESULT 970
 ID AL03616 Standard; DNA; 32191 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 6304.
 PN WO200155320-A2.
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 32191;
 Best Local Similarity 82.4%; Pred. No. 8.8e-46;
 RESULT 971
 ID ABA07814 Standard; DNA; 32191 BP.

DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 609.
 PN WO200155320-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 32191;
 Best Local Similarity 82.4%; Pred. No. 8.8e-46;

RESULT 972
 ID ABA20618 Standard; DNA; 32220 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 12949.
 PN WO20015903-A2.

PD 16-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 5; Length 32220;
 Best Local Similarity 80.1%; Pred. No. 8.8e-46;

RESULT 973
 ID ABX61804 Standard; DNA; 40645 BP.
 DE Genomic DNA encoding novel human GABA transporter related protein.
 PN US2002142381-A1.
 PD 03-OCT-2002.

PA (GONG/) GONG F.
 PA (KETC/) KETCHUM K A.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY B M.
 Query Match 21.8%; Score 198; DB 8; Length 40645;
 Best Local Similarity 76.7%; Pred. No. 9.6e-46;

RESULT 974
 ID ADA49717 Standard; DNA; 40645 BP.
 DE Genomic DNA encoding human transporter protein.
 Query Match 21.8%; Score 198; DB 9;
 Best Local Similarity 76.7%; Pred. No. 9.6e-46;

RESULT 975
 ID AAK7437 Standard; DNA; 52845 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26249.
 PN WO200157182-A2.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 8; Length 52845;
 Best Local Similarity 83.5%; Pred. No. 1.1e-45;

RESULT 976
 ID ACM44918 Standard; DNA; 59514 BP.
 DE Human genomic sequence HQG20493.
 PN WO2003073826-A2.
 PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 198; DB 11; Length 55114;
 Best Local Similarity 82.4%; Pred. No. 1.1e-45;

RESULT 977
 ID ADA05684 Standard; DNA; 59817 BP.
 DE Human DUSP10 carcinoma associated gene, SEQ ID NO:1202.
 PN WO2003057146-A2.
 PD 17-JULY-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 198; DB 9; Length 59817;
 Best Local Similarity 82.6%; Pred. No. 1.1e-45;

RESULT 978
 ID ADB72422 Standard; DNA; 59817 BP.
 DE Human DUSP10 Gene.
 PN WO2003010583-A2.
 PD 30-JAN-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 198; DB 10; Length 59817;
 Best Local Similarity 82.6%; Pred. No. 1.1e-45;

RESULT 979
 ID ADE05932 Standard; DNA; 59817 BP.
 DE Human DUSP10 gene, genomic DNA sequence.
 PN WO2003039184-A2.
 PD 15-MAY-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 198; DB 10; Length 59817;
 Best Local Similarity 82.6%; Pred. No. 1.1e-45;

RESULT 980
 ID AAD43934 Standard; DNA; 70000 BP.
 DE Human phospholipase A2 (PLA2), group VI (Ca2+-independent) gene.

PN US6410325-B1.
 PD 22-JUN-2002.
 PA (ISIS-) ISIS PHARM INC. 21.8%; Score 198; DB 6; Length 70000;
 Best Local Similarity 80.1%; Pred. No. 1.2e-45;
 RESULT 981
 ID ACN44938 standard; DNA; 73771 BP.
 DE Human genomic sequence hCG3739A.
 PN WO2003073126-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 198; DB 11; Length 73771;
 Best Local Similarity 82.8%; Pred. No. 1.2e-45;
 RESULT 982
 ID AAL57572 standard; cDNA; 107818 BP.
 DE Human Phosphomannomutase 1 cDNA.
 PN WO2003059118-A2.
 PD 24-JUN-2003.
 PA (GENE-) GENE LOGIC INC.
 PA (IGBL-) LG BIOMEDICAL INST.
 Best Local Similarity 21.8%; Score 198; DB 9; Length 107818;
 RESULT 983
 Query Match 21.8%; Score 198; DB 10; Length 11000;
 Best Local Similarity 75.1%; Pred. No. 1.4e-45;
 RESULT 984
 Query Match 21.8%; Score 198; DB 10; Length 11000;
 Best Local Similarity 75.1%; Pred. No. 1.4e-45;
 RESULT 985
 ID ADQ19183 standard; DNA; 110665 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2002.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Best Local Similarity 21.8%; Score 198; DB 12; Length 110665;
 RESULT 986
 ID ADQ17641 standard; DNA; 114771 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 458.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Best Local Similarity 21.8%; Score 198; DB 12; Length 114771;
 RESULT 987
 ID ADQ97119 standard; DNA; 117829 BP.
 DE Human cancer associated sequence HD08-031, SEQ ID 296.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.8%; Score 198; DB 12; Length 117829;
 Best Local Similarity 76.0%; Pred. No. 1.4e-45;
 RESULT 988
 ID ADH63063 standard; DNA; 132762 BP.
 DE Human fibroblast growth factor receptor 2 related sequence, SEQ ID 17.
 PN WO2003024987-A1.
 PD 27-MAR-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.8%; Score 198; DB 10; Length 132762;
 Best Local Similarity 82.6%; Pred. No. 1.5e-45;
 RESULT 989
 ID ABK84979 standard; cDNA; 149671 BP.
 DE Human cDNA differentially expressed in granulocytic cells #1368.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 21.8%; Score 198; DB 6; Length 149671;
 Best Local Similarity 83.8%; Pred. No. 1.6e-45;
 RESULT 990
 ID ADB70361 standard; cDNA; 149671 BP.
 DE Mobsin cDNA SEQ ID NO:53.
 PN WO200301229-A2.
 PD 13-MAR-2003.

PA (BGHM-) BRIGHAM & WOMENS HOSPITAL INC. 21.8%; Score 198; DB 9; Length 149671;
 Best Local Similarity 83.8%; Pred. No. 1.6e-45;
 RESULT 991
 ID ADJ37140 standard; cDNA; 149671 BP.
 DE Human malignant pleural mesothelioma (NPM) cDNA #23.
 PN US2003219760-A1.
 PD 27-NOV-2003.
 PA (BGHM-) BRIGHAM & WOMENS HOSPITAL INC. 21.8%; Score 198; DB 12; Length 149671;
 Best Local Similarity 83.8%; Pred. No. 1.6e-45;
 RESULT 992
 ID ADL1752 standard; DNA; 190000 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #284.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC. 21.8%; Score 198; DB 10; Length 190000;
 Best Local Similarity 81.2%; Pred. No. 1.7e-45;
 RESULT 993
 ID ADF14037 standard; DNA; 1167 BP.
 DE Human endometrial-specific DNA - SEQ ID 2.
 PN WO2003059327-A1.
 PD 24-JUL-2003.
 PA (DIAD-) DIADEXUS INC. 21.8%; Score 197.8; DB 10; Length 1167;
 Best Local Similarity 75.7%; Pred. No. 2.8e-46;
 RESULT 994
 ID AAC69633 standard; cDNA; 1295 BP.
 DE Human secreted protein gene 37 SEQ ID NO:47.
 PN WO200506882-A1.
 PD 28-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC. 21.8%; Score 197.8; DB 3; Length 1295;
 Best Local Similarity 77.5%; Pred. No. 2.9e-46;
 RESULT 995
 ID ABK35888 standard; cDNA; 3705 BP.
 DE cDNA sequence #279 encoding novel human secreted protein.
 PN WO200177289-A2.
 PD 18-OCT-2001.
 PA (GEMY-) GENETICS INST INC. 21.8%; Score 197.8; DB 6; Length 3705;
 Best Local Similarity 78.0%; Pred. No. 4.3e-46;
 RESULT 996
 ID AAL5735 standard; cDNA; 6610 BP.
 DE Human polynucleotide SEQ ID NO 138.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC. 21.8%; Score 197.8; DB 4; Length 6610;
 Best Local Similarity 82.1%; Pred. No. 5.4e-46;
 RESULT 997
 ID AXK5163 standard; cDNA; 7005 BP.
 DE Human Polynucleotide SEQ ID NO 181.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC. 21.8%; Score 197.8; DB 4; Length 7005;
 Best Local Similarity 82.1%; Pred. No. 5.6e-46;
 RESULT 998
 ID AX58051 standard; DNA; 16707 BP.
 DE Genomic DNA for Human GABAB receptors.
 PN WO9921190-A1.
 PD 06-MAY-1999.
 PA (ASTR-) ASTRA AB. 21.8%; Score 197.8; DB 2; Length 16707;
 Best Local Similarity 80.7%; Pred. No. 7.8e-46;
 RESULT 999
 ID AAI0377 standard; DNA; 21913 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 6065.
 PN WO20015320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 21.8%; Score 197.8; DB 4; Length 21913;
 Best Local Similarity 77.9%; Pred. No. 8.6e-46;

RESULT 1000
 ID AAL03378 standard; DNA; 21913 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 6066.
 PN WO200155320-A2.
 PD 02-AUG-2001.

Query Match 21.8%; Score 197.8; DB 4; Length 21913;
 Best Local Similarity 77.9%; Pred. No. 8.6e-46;

RESULT 1001
 ID AAL0379 standard; DNA; 21913 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 6067.
 PN WO200155320-A2.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 21913;
 Best Local Similarity 77.9%; Pred. No. 8.6e-46;

RESULT 1002
 ID AAK70624 standard; DNA; 24768 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 25436.
 PN WO200157182-A2.

PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 21913;
 Best Local Similarity 77.9%; Pred. No. 8.6e-46;

RESULT 1003
 ID ADI181379 standard; DNA; 25001 BP.
 DE Human P2X4 genomic DNA sequence.
 PN US2004002152-A1.

PD 01-JAN-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 24768;
 Best Local Similarity 76.9%; Pred. No. 9.e-46;

RESULT 1004
 ID ADH36221 standard; DNA; 28616 BP.
 DE Human purinergic receptor P2X4 gene sequence.
 PN WO2003101177-A2.

PD 11-DEC-2003.
 PA (SEQUO-) SQUEONOM INC.
 Query Match 21.8%; Score 197.8; DB 12; Length 28616;
 Best Local Similarity 76.9%; Pred. No. 9.6e-46;

RESULT 1005
 ID AAS33492 standard; DNA; 32191 BP.
 DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 446.
 PN WO200155319-A2.

PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.8; DB 12; Length 28616;
 Best Local Similarity 77.5%; Pred. No. 1.e-45;

RESULT 1006
 ID ACN44490 standard; DNA; 32865 BP.
 DE Human genomic Sequence hCG253/5.
 PN WO2003073826-A2.

PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 197.8; DB 11; Length 32865;
 Best Local Similarity 78.5%; Pred. No. 1.e-45;

RESULT 1007
 ID AAK1918 standard; DNA; 42048 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 26730.
 PN WO200157182-A2.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 42048;
 Best Local Similarity 79.6%; Pred. No. 1.1e-45;

RESULT 1008
 ID AAC6140 standard; DNA; 50000 BP.
 DE Nucleotide sequence of a beta-tubulin antigen.
 PN WO20050593-A1.

PD 31-AUG-2000.
 PA (UYTE-) UNIV TENNESSEE RES CORP.
 Query Match 21.8%; Score 197.8; DB 3; Length 50000;

Best Local Similarity 81.7%; Pred. No. 1.2e-45;
 RESULT 1009
 ID ADD3228 standard; DNA; 53522 BP.
 DE Human PKD1 gene.
 PN WO200206529-A2.

PD 24-JUN-2002.
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 Query Match 21.8%; Score 197.8; DB 6; Length 53522;
 Best Local Similarity 80.5%; Pred. No. 1.2e-45;

RESULT 1010
 ID AAT94101 standard; DNA; 53526 BP.
 DE Human PKD1 gene.
 PN WO974457-A1.

PD 27-NOV-1997.
 PA (GENZ-) GENZYME CORP.
 Query Match 21.8%; Score 197.8; DB 2; Length 53526;
 Best Local Similarity 80.5%; Pred. No. 1.2e-45;

RESULT 1011
 ID AAT18551 standard; DNA; 53577 BP.
 DE Human polycystic kidney disease normal PKD1 gene.
 PN WO9612033-A1.

PD 25-APR-1996.
 PA (IGIG-) IIG LAB INC.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 21.8%; Score 197.8; DB 2; Length 53577;
 Best Local Similarity 80.5%; Pred. No. 1.2e-45;

RESULT 1012
 ID AAT94108 standard; DNA; 53577 BP.
 DE Human PKD1 locus between chromosomal markers ATP1 (ATP6C) and D16S84.
 PN WO974457-A1.

PD 27-NOV-1997.
 PA (GENZ-) GENZYME CORP.
 Query Match 21.8%; Score 197.8; DB 2; Length 53577;
 Best Local Similarity 80.5%; Pred. No. 1.2e-45;

RESULT 1013
 ID AAK3212 standard; DNA; 68356 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 38024.
 PN WO200157182-A2.

PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 68356;
 Best Local Similarity 80.5%; Pred. No. 1.3e-45;

RESULT 1014
 ID AAK6723 standard; DNA; 68356 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 22095.
 PN WO200157182-A2.

PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 68356;
 Best Local Similarity 80.5%; Pred. No. 1.3e-45;

RESULT 1015
 ID ACN44710 standard; DNA; 70242 BP.
 DE Human genomic Sequence hCG1784894.
 PN WO2003073826-A2.

PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 197.8; DB 11; Length 70242;
 Best Local Similarity 80.7%; Pred. No. 1.3e-45;

RESULT 1016
 ID ADR33001 standard; DNA; 96256 BP.
 DE Drug therapy altered expressed gene #352.
 PN WO2004072265-A2.

PD 26-AUG-2004.
 PA (AMHP-) WYETH.
 PA (BURC-) BURCZINSKI M.
 PA (TWIN-) TWINB N.
 PA (DORN-) DORNER A. J.
 PA (TRIP-) TRIPICCHIO W L.
 Query Match 21.8%; Score 197.8; DB 13; Length 96256;
 Best Local Similarity 80.7%; Pred. No. 1.5e-45;

RESULT 1017
 ID ABK12169 standard; DNA; 98690 BP.
 DE Human DNA representing the Tachykinin Receptor 1, TACR1, gene.

DE Human IDE/KNSLI gene DNA sequence SeqID484.
 PN US200321380-A1.
 PD 04-DEC-2003.

PA (GEHO-) GEN HOSPITAL CORP.
 Query Match 21.8%; Score 197.8; DB 12; Length 202100;
 Best Local Similarity 79.6%; Pred. No. 2e-45;

RESULT 1027
 ID ABP6352 standard; DNA; 300000 BP.
 DE Human PTEN1 genomic DNA sequence SEQ ID NO:33.
 PN WO2003029322-A2.

PD 10-APR-2003.
 PA (MOUN-) MOUNT SINAI SCHOOL MEDICINE.
 Query Match 21.8%; Score 197.8; DB 10; Length 300000;
 Best Local Similarity 82.3%; Pred. No. 2.4e-45;

RESULT 1028
 ID ADQ14076 standard; DNA; 300001 BP.
 DE Human protein tyrosine phosphatase 11 gene sequence SEQ ID NO:33.
 PN WO200401216-A2.

PD 21-MAY-2004.
 PA (MOUN-) MOUNT SINAI SCHOOL MEDICINE.
 Query Match 21.8%; Score 197.8; DB 12; Length 300001;
 Best Local Similarity 82.3%; Pred. No. 2.4e-45;

RESULT 1029
 ID ASX43104 standard; DNA; 325791 BP.
 DE Human Oestrogen receptor beta gene.
 PN WO200462793-A2.

PD 30-AUG-2001.
 PA (PEKE-) PB CORP NY.
 Query Match 21.8%; Score 197.8; DB 4; Length 325791;
 Best Local Similarity 84.5%; Pred. No. 2.4e-45;

RESULT 1030
 ID ABX6184 standard; DNA; 601 BP.
 DE Novel human transporter protein related polynucleotide #40.
 PN US2002142381-A1.

PD 03-OCT-2002.
 PA (GONG/) GONG F.
 PA (KETC/) KETCHUM K A.
 PA (DFRA/) DI FRANCESCO V.
 PA (BRAS/) BEASLEY B M.
 Query Match 21.8%; Score 197.6; DB 8; Length 601;
 Best Local Similarity 76.4%; Pred. No. 2.5e-66;
 RESULT 1031
 ID ABX61842 standard; DNA; 601 BP.
 DE Novel human transporter protein related polynucleotide #38.
 PN US2002142381-A1.

PD 03-OCT-2002.
 PA (GONG/) GONG F.
 PA (KETC/) KETCHUM K A.
 PA (DFRA/) DI FRANCESCO V.
 PA (BRAS/) BEASLEY B M.
 Query Match 21.8%; Score 197.6; DB 8; Length 601;
 Best Local Similarity 76.4%; Pred. No. 2.5e-46;

RESULT 1032
 ID ADP3033 standard; cDNA; 993 BP.
 DE Human cancer suppressing protein PP12616-encoding cDNA, SEQ:25 and 27.
 PN CN1368108-A.
 PD 11-SEP-2002.
 PA (SHAN-) SHANGHAI INST ONCOLOGY.
 Query Match 21.8%; Score 197.6; DB 10; Length 993;
 Best Local Similarity 77.0%; Pred. No. 3e-46;

RESULT 1033
 ID AHH14398 Standard; cDNA; 2182 BP.
 DE Human cDNA Sequence SEQ ID NO:11832.
 PN EP1074617-A2.

PD 07-FEB-2001.
 PA (HBLI-) HELIX RES INST.
 Query Match 21.8%; Score 197.6; DB 4; Length 2182;
 Best Local Similarity 84.3%; Pred. No. 4e-46;

RESULT 1034
 ID ABK35751 standard; cDNA; 2702 BP.
 DE cDNA sequence #112 encoding novel human secreted protein.
 PN WO200177289-A2.

PA (GENE-) GEN HOSPITAL CORP.
 Query Match 21.8%; Score 197.8; DB 10; Length 202100;
 Best Local Similarity 77.6%; Pred. No. 2e-45;

RESULT 1026
 ID ADH54357 standard; DNA; 202100 BP.

PD 18-OCT-2001. PA (HUMA-) HUMAN GENOME SCI INC.
 PA Query Match 21.8%; Score 197.6; DB 6; Length 2702;
 Best Local Similarity 77.1%; Pred. No. 1e-45;
 RESULT 1035 ID ADI9476 standard; DNA; 23626 BP.
 DE Human respiratory system associated polypeptide-related DNA SeqID940.
 ID ABV593 standard; DNA; 3509 BP.
 DE Novel human gene #6.
 PN WO200577255-A1.
 PD 03-OCT-2002. PA (HISB-) HISBQ INC.
 PA Query Match 21.8%; Score 197.6; DB 10; Length 3509;
 Best Local Similarity 84.3%; Pred. No. 4.9e-16;
 RESULT 1036 ID AAK8053 standard; DNA; 5331 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37865.
 PN WO2005157182-A2.
 PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC.
 PA Query Match 21.8%; Score 197.6; DB 4; Length 3531;
 Best Local Similarity 80.5%; Pred. No. 5.7e-46;
 RESULT 1037 ID AAK8051 standard; DNA; 7022 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37863.
 PN WO2005157182-A2.
 PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC.
 PA Query Match 21.8%; Score 197.6; DB 4; Length 7022;
 Best Local Similarity 80.5%; Pred. No. 6.3e-46;
 RESULT 1038 ID AAK8820 standard; DNA; 11840 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38632.
 PN WO2005157182-A2.
 PD 09-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC.
 PA Query Match 21.8%; Score 197.6; DB 4; Length 11840;
 Best Local Similarity 76.4%; Pred. No. 7.8e-46;
 RESULT 1039 ID AAS20506 standard; DNA; 23626 BP.
 DE Genomic sequence #346 encoding for novel human respiratory antigen.
 PN WO2005155448-A1.
 PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC.
 PA Query Match 21.8%; Score 197.6; DB 4; Length 23626;
 Best Local Similarity 77.1%; Pred. No. 1e-45;
 RESULT 1040 ID ABA21480 standard; DNA; 23626 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 13812.
 PN WO2005159033-A2.
 PD 16-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC.
 PA Query Match 21.8%; Score 197.6; DB 5; Length 23632;
 Best Local Similarity 77.1%; Pred. No. 1e-45;
 RESULT 1041 ID AAS2997 standard; DNA; 23626 BP.
 DE Human lung antigen genomic DNA #68.
 PN WO2005159033-A2.
 PD 20-MAR-2003. PA (HUMA-) HUMAN GENOME SCI INC.
 PA Query Match 21.8%; Score 197.6; DB 5; Length 23632;
 Best Local Similarity 77.1%; Pred. No. 1e-45;
 RESULT 1042 ID ADB3335 standard; DNA; 23632 BP.
 DE Human novel lung related polypeptide DNA SEQ ID NO 262.
 PN WO2005155303-A2.
 PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI INC.
 PA Query Match 21.8%; Score 197.6; DB 5; Length 23626;
 Best Local Similarity 77.1%; Pred. No. 1e-45;
 RESULT 1043 ID ADG41703 standard; DNA; 23632 BP.
 DE Human respiratory system associated genomic DNA seq id 941.
 PN US2003215693-A1.
 PD 20-NOV-2003. PA (HUMA-) HUMAN GENOME SCI INC.
 PA Query Match 21.8%; Score 197.6; DB 10; Length 23632;
 Best Local Similarity 77.1%; Pred. No. 1e-45;
 RESULT 1044 ID ADI477 standard; DNA; 23632 BP.
 DE Human respiratory system associated polypeptide-related DNA SeqID941.
 PN US200307704-A1.
 PD 24-APR-2003. PA (HUMA-) HUMAN GENOME SCI INC.
 PA Query Match 21.8%; Score 197.6; DB 11; Length 23632;
 Best Local Similarity 77.1%; Pred. No. 1e-45;
 RESULT 1051 ID ADI5710 standard; DNA; 29040 BP.
 DE Human genomic sequence for LFNG.
 PN US200321558-A1.
 PD 20-NOV-2003. PA (MORR-) MORRIS D W.
 PA (ENGE-) ENGERLICH E K.
 PA Query Match 21.8%; Score 197.6; DB 11; Length 29040;
 Best Local Similarity 84.3%; Pred. No. 1.1e-45;
 RESULT 1052 ID ADA03092 standard; DNA; 29322 BP.
 DE Human LFNG carcinoma associated gene, SEQ ID NO:1610.
 PN WO2003057146-A2.
 PD 20-NOV-2003.

PA (SAGR-) SAGRES DISCOVERY. Query Match 21.8%; Score 197.6; DB 9; Length 29322; Best Local Similarity 84.3%; Pred. No. 1.1e-45; DE Human LFNG gene genomic DNA sequence. PN WO2003053224-A2.

PD 03-JUL-2003.

PA (SAGR-) SAGRES DISCOVERY. Query Match 21.8%; Score 197.6; DB 9; Length 29322; Best Local Similarity 84.3%; Pred. No. 1.1e-45; DE Human LFNG gene. PN WO2003008503-A2.

PD 30-JAN-2003.

PA (SAGR-) SAGRES DISCOVERY. Query Match 21.8%; Score 197.6; DB 10; Length 29322; Best Local Similarity 84.3%; Pred. No. 1.1e-45; DE Human immune/baematoopoietic antigen genomic sequence SEQ ID NO:23489. PN WO2003517182-A2.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.8%; Score 197.6; DB 4; Length 34269; Best Local Similarity 74.4%; Pred. No. 1.2e-45; DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39980.

RESULT 1055

ID AAK68677 standard; DNA; 34269 BP.

DB Human immune/baematoopoietic antigen genomic sequence SEQ ID NO:23489.

RESULT 1056

ID AAK85168 standard; DNA; 34269 BP.

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39980.

PN WO2003517182-A2.

PD 09-AUG-2001.

PA (HOMA-) HUMAN GENOME SCI INC. Query Match 21.8%; Score 197.6; DB 4; Length 34269; Best Local Similarity 74.4%; Pred. No. 1.2e-45; DE Tumour treatment-related human gene sequence SeqID76. PN WO2004034995-A2.

RESULT 1057

ID AUS88040 standard; DNA; 37797 BP.

DE Human genomic sequence hCG38101.

PN WO2003073826-A2.

RESULT 1058

ID ACM44534 standard; DNA; 39768 BP.

DE Human genomic sequence hCG38101.

PN WO2003073826-A2.

PA (IUPI-) UNIV PITTSBURGH. Query Match 21.8%; Score 197.6; DB 13; Length 37797; Best Local Similarity 80.3%; Pred. No. 1.2e-45; DE Human NAC nucleotide sequence SEQ ID NO:10.

RESULT 1059

ID ABD3318 standard; DNA; 52987 BP.

DE Human cancer-associated (CA) gene HD07-057.

PN WO2004058146-A2.

PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY. Query Match 21.8%; Score 197.6; DB 11; Length 39768; Best Local Similarity 78.1%; Pred. No. 1.2e-45; DE Human sulfatase SULF1 gene. PN WO2004058146-A2.

RESULT 1060

ID ACC45150 standard; DNA; 96649 BP.

DE Human NAC nucleotide sequence SEQ ID NO:10.

PN WO2003024988-A1.

PD 27-MAR-2003.

PA (ISIS-) ISIS PHARM INC. Query Match 21.8%; Score 197.6; DB 13; Length 52987; Best Local Similarity 77.1%; Pred. No. 1.4e-45; DE Human NAC nucleotide sequence SEQ ID NO:10.

RESULT 1061

ID ACC45150 standard; DNA; 96649 BP.

DE Human NAC nucleotide sequence SEQ ID NO:10.

PN WO2003024988-A1.

RESULT 1062

Query Match 21.8%; Score 197.6; DB 10; Length 110000; Best Local Similarity 73.6%; Pred. No. 1.8e-45; DE Human kinase genomic DNA. PN US2003073623-A1.

PD 17-APR-2003.

PA (DRMA/) DRMANAC R T. Query Match 21.8%; Score 197.6; DB 12; Length 110000; Best Local Similarity 73.6%; Pred. No. 1.8e-45;

RESULT 1063

ID ACA64961 standard; DNA; 152141 BP.

DE Human BCR DNA corresponding to U07000. PN DB10127572-A1.

PD 05-DEC-2002.

PA (PATH-) PATHOARRAY GMBH. Query Match 21.8%; Score 197.6; DB 8; Length 152141; Best Local Similarity 84.0%; Pred. No. 2.1e-45; DE Human cDNA differentially expressed in granulocytic cells #142. PN WO20028999-A2.

PD 11-APR-2002.

PA (GENB-) GENE LOGIC INC. Query Match 21.8%; Score 197.6; DB 6; Length 175737; Best Local Similarity 76.6%; Pred. No. 2.2e-45; DE Osteoarthritis-associated polymorphic nucleotide #128. PN WO2003054166-A2.

PD 03-JUL-2003.

PA (INCY-) INCYTE GENOMICS INC. Query Match 21.8%; Score 197.6; DB 10; Length 175737; Best Local Similarity 76.6%; Pred. No. 1.1e-45; DE Osteoarthritis-associated polymorphic nucleotide #128. PN WO2003054166-A2.

RESULT 1065

ID ADL13595 standard; DNA; 175737 BP.

DE Osteoarthritis-associated polymorphic nucleotide #128. PN WO2003054166-A2.

PD 03-JUL-2003.

PA (PROT-) PROTEIN DESIGN LABS INC. Query Match 21.8%; Score 197.6; DB 12; Length 175737; Best Local Similarity 76.6%; Pred. No. 2.2e-45; DE Human genomic sequence hCG38101.

RESULT 1066

ID ADU18234 standard; DNA; 175737 BP.

DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1753. PN WO2004048938-A2.

PD 10-JUN-2004.

PA (RBCG-) UNIV CALIFORNIA. Query Match 21.8%; Score 197.6; DB 12; Length 175737; Best Local Similarity 76.6%; Pred. No. 2.2e-45; DE Human SULF2 genomic DNA sequence. PN WO2003073827-A2.

PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY. Query Match 21.8%; Score 197.6; DB 11; Length 198522; Best Local Similarity 78.7%; Pred. No. 2.3e-45; DE Human genomic sequence hCG38101.

RESULT 1068

ID AB55554 standard; DNA; 260209 BP.

DE Human SULF2 genomic DNA sequence. PN WO200289327-A2.

PD 01-AUG-2002.

PA (RBCG-) UNIV CALIFORNIA. Query Match 21.8%; Score 197.6; DB 6; Length 260209; Best Local Similarity 86.9%; Pred. No. 2.6e-45; DE Human SULF2 genomic DNA sequence. PN WO200289327-A2.

PD 11-APR-2004.

PA (RBCG-) UNIV CALIFORNIA. Query Match 21.8%; Score 197.6; DB 12; Length 260209; Best Local Similarity 86.9%; Pred. No. 2.6e-45; DE Human Sulfatase SULF1 gene. PN WO2004051365-A2.

PD 11-APR-2004.

PA (RBCG-) UNIV CALIFORNIA. Query Match 21.8%; Score 197.6; DB 6; Length 326014; Best Local Similarity 86.9%; Pred. No. 2.6e-45; DE Human gene for novel serine/threonine serine kinase. PN WO2004051365-A2.

RESULT 1070

ID ABK89296 standard; DNA; 326014 BP.

DE Human gene for novel serine/threonine serine kinase. PN WO2004051365-A2.

PD 11-APR-2004.

PA (RBCG-) UNIV CALIFORNIA. Query Match 21.8%; Score 197.6; DB 6; Length 326014; Best Local Similarity 86.9%; Pred. No. 2.6e-45; DE Human gene for novel serine/threonine serine kinase. PN WO2004051365-A2.

RESULT 1071

ID ADQ94981 standard; DNA; 326014 BP.

DE Human kinase genomic DNA. PN WO2004051365-A2.

PD 11-APR-2004.

PA (RBCG-) UNIV CALIFORNIA. Query Match 21.8%; Score 197.6; DB 12; Length 326014; Best Local Similarity 86.9%; Pred. No. 2.6e-45; DE Human kinase genomic DNA. PN WO2004051365-A2.

RESULT 1072

ID ACT36634 standard; cDNA; 463 BP.

DE Human endothelial cell cDNA #4767. PN US2003073623-A1.

PD 17-APR-2003.

PA (DRMA/) DRMANAC R T.

PA (LABA-) LABAT I.
 PA (STAC-) STACHE-CRAIN B.
 PA (DICK-) DICKSON M C.
 PA (JONE-) JONES L W.
 Query Match Best Local Similarity 84.8%; Score 197.4; DB 9; Length 463;
 RESULT 1073
 ID ADB83200 standard; cDNA; 588 BP.
 DE Human CDNA sequence useful for the treatment of cancer (SeqID 1413).
 PN WO200305226-A2.
 PD 19-JUN-2003.
 PA (CHIR-) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 Query Match Best Local Similarity 85.0%; Pred. No. 2.8e-46;
 Best Local Similarity 85.0%; Pred. No. 2.8e-46;
 RESULT 1074
 ID AAH9452 standard; cDNA; 874 BP.
 DE Human EST-derived coding sequence SEQ ID NO: 309.
 PN WO200354477-A2.
 PD 02-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match Best Local Similarity 84.8%; Score 197.4; DB 4; Length 874;
 RESULT 1075
 ID ADG10849 standard; cDNA; 1599 BP.
 DE Human STAT6-activating protein-encoding cDNA, SEQ ID NO:439.
 PN WO200296933-A1.
 PD 05-DEC-2002.
 PA (ASAH-) ASAMI KASEI KOGYO KK.
 Query Match Best Local Similarity 84.8%; Score 197.4; DB 10; Length 1599;
 RESULT 1076
 ID AAK75880 standard; DNA; 3891 BP.
 DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:30700.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 82.3%; Pred. No. 5.8e-46;
 RESULT 1077
 ID AAK90709 standard; DNA; 5032 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 4285.
 PN WO200155334-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 84.8%; Score 197.4; DB 4; Length 5032;
 RESULT 1078
 ID ABD3436 standard; DNA; 52710 BP.
 DE Human cancer-associated (CA) gene RD07-082.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match Best Local Similarity 82.1%; Pred. No. 1.6e-45;
 RESULT 1079
 ID ABD3470 standard; DNA; 61765 BP.
 DE Human cancer-associated (CA) gene RD07-090.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match Best Local Similarity 80.5%; Pred. No. 1.7e-45;
 RESULT 1080
 ID ACN44362 standard; DNA; 68255 BP.
 DE Human genomic sequence hcc39597.
 PN WO200307326-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match Best Local Similarity 73.3%; Score 197.4; DB 11; Length 68255;
 RESULT 1081
 Query Match Best Local Similarity 82.6%; Score 197.4; DB 6; Length 110000;
 Query Match Best Local Similarity 82.6%; Pred. No. 5.2e-46;

PA Best Local Similarity 84.8%; Pred. No. 2.1e-45;
 RESULT 1082
 ID ABN61073 standard; cDNA; 662 BP.
 DE Human cancer related polynucleotide SEQ ID NO 1040.
 PN WO200214500-A2.
 PD 21-FEB-2002.
 PA (CHIR-) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 Query Match Best Local Similarity 82.0%; Pred. No. 3.3e-46;
 RESULT 1083
 ID ACC86725 standard; DNA; 751 BP.
 DE Human VEGFR-1 nucleotide sequence SEQ ID NO:20.
 PN WO200302227-A2.
 PD 20-MAR-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match Best Local Similarity 74.8%; Pred. No. 3.5e-46;
 RESULT 1084
 ID AAH16580 standard; cDNA; 2092 BP.
 DE Human cDNA sequence SEQ ID NO:15661.
 PN BP104617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match Best Local Similarity 82.7%; Score 197.2; DB 4; Length 2092;

RESULT 1094
 ID ADP81697 standard; DNA; 4908 BP.
 DE Leukaemia-related DNA sequence #2253.
 PN WO200303443-A2.
 PD 15-MAY-2003.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
 PA (HAFE-) HAERLACH T.
 PA (SCHO/) SCHIOCH C.
 PA (KERN/) KERN W.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 10; Length 4908;
 RESULT 1095
 ID ADP81698 standard; DNA; 4908 BP.
 DE Leukaemia-related DNA sequence #2254.
 PN WO200303443-A2.
 PD 15-MAY-2003.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
 PA (HAFE-) HAERLACH T.
 PA (SCHO/) SCHIOCH C.
 PA (KERN/) KERN W.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 10; Length 4908;
 RESULT 1096
 ID AAK73007 standard; DNA; 6658 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27819.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 4; Length 6658;
 RESULT 1097
 ID AAL03021 standard; DNA; 6658 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 5709.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 4; Length 6658;
 RESULT 1098
 ID AAL06167 standard; DNA; 8577 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 8855.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 4; Length 8577;
 RESULT 1099
 ID ABL98732 standard; DNA; 8577 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3384.
 PN WO200155317-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 4; Length 8577;
 RESULT 1100
 ID ABL98732 standard; DNA; 8577 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 9378.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 5; Length 8577;
 RESULT 1101
 ID ABL98747 standard; DNA; 8577 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 9378.
 PN WO200159063-A2.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 5; Length 8577;
 RESULT 1102
 ID AAK8986 standard; DNA; 32224 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3562.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 4; Length 32224;
 RESULT 1102
 Best Local Similarity 84.2%; Pred. No. 1.5e-45;

ID ABD33190 standard; DNA; 33478 BP.
 DE Human cancer-associated (CA) gene HD07-028.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 13; Length 33478;
 RESULT 1103
 ID ABN9630 standard; DNA; 40433 BP.
 DE Gene #3328 used to diagnose liver cancer.
 PN WO2003039443-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 6; Length 40433;
 Best Local Similarity 80.5%; Pred. No. 1.6e-45;
 RESULT 1104
 ID ADA02528 standard; DNA; 57763 BP.
 DE Human MIB carcinoma associated gene, SEQ ID NO:1046.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 9; Length 57763;
 RESULT 1105
 ID ADB72266 standard; DNA; 57763 BP.
 DE Human MYB gene.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 10; Length 57763;
 RESULT 1106
 ID ADB95776 standard; DNA; 57763 BP.
 DE Human MYB gene Genomic DNA sequence.
 PN WO2003039444-A2.
 PD 15-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 10; Length 57763;
 RESULT 1107
 ID ADU53477 standard; DNA; 70000 BP.
 DE Human PPP3CB genomic DNA #3.
 PN US20040423382-A1.
 PD 05-FEB-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 12; Length 70000;
 RESULT 1108
 ID AAK85590 standard; DNA; 75384 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40402.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 4; Length 75384;
 RESULT 1109
 ID ADD31364 standard; DNA; 92139 BP.
 DE 920b gene fragment in human chromosome 17 at 17q21.
 PN WO2002010455-A2.
 PD 07-FEB-2002.
 PA (CBL-) CELITECH R & D INC.
 PA (STRA-) STRABLING HAMPTON K.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 6; Length 92139;
 RESULT 1110
 ID ADD324 standard; DNA; 56571 BP.
 DE Human chromosome 3 q-arm breakpoint region.
 PN WO20020541-A1.
 PD 14-NOV-2002.
 PA (MORD-) MURDOCH CHILDRENS RES INST.
 PA (DELA-) DELATYCKI M.
 Query Match Best Local Similarity 21.7%; Score 197.2; DB 8; Length 110000;

RESULT 1111
 Query Match 21.7%; Score 197.2; DB 11; Length 110000;
 Best Local Similarity 78.9%; Pred. No. 2.4e-45;
 RESULT 1112
 Query Match 21.7%; Score 197.2; DB 11; Length 110000;
 Best Local Similarity 78.9%; Pred. No. 2.4e-45;

RESULT 1113
 Query Match 21.7%; Score 197.2; DB 11; Length 110000;
 Best Local Similarity 74.0%; Pred. No. 2.4e-45;

RESULT 1114
 ID ADH76549 standard; DNA; 122557 BP.
 DE Melan-concentrating hormone receptor 1 locus clone.
 PN WO200310449-A2.

PD 18-DEC-2003.

PA (UYPH-) UNIV PHILIPS MARBURG.
 Query Match 21.7%; Score 197.2; DB 12; Length 122557;
 Best Local Similarity 78.6%; Pred. No. 2.5e-45;

RESULT 1115
 ID ADQ80354 standard; cDNA; 127145 BP.
 DE Hermansky-Pudlak syndrome associated cDNA.
 PN WO2004063709-A2.

PD 29-JUL-2004.

PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
 Query Match 21.7%; Score 197.2; DB 12; Length 122557;
 Best Local Similarity 78.6%; Pred. No. 2.5e-45;

RESULT 1116
 ID ADP1613 standard; DNA; 130320 BP.
 DE Human sclerostin gene region.
 PN WO2003087763-A2.

PD 23-OCT-2003.

PA (CBLL-) CELITECH R & D INC.
 (TYRO-) UNIV ROTTERDAM ERASMUS.
 Query Match 21.7%; Score 197.2; DB 10; Length 130320;
 Best Local Similarity 80.5%; Pred. No. 2.5e-45;

RESULT 1117
 ID ADQ97183 standard; DNA; 138627 BP.
 DE Human cancer associated sequence HD08-011, SEQ ID 159.
 PN WO2004060304-A2.

PD 22-JUN-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 197.2; DB 12; Length 138627;
 Best Local Similarity 84.5%; Pred. No. 2.5e-45;

RESULT 1118
 ID AA195194 standard; cDNA; 717 BP.
 DE Human neuroblastoma expressed polynucleotide SEQ ID NO 1269.
 PN WO200166719-A1.

PD 13-SEP-2001.

PA (CHIB-) CHIBA PREFECTURE.
 PA (HISM-) HISAMITSU PHARM CO LTD.
 Query Match 21.7%; Score 197; DB 4; Length 717;
 Best Local Similarity 75.1%; Pred. No. 3.9e-46;

RESULT 1119
 ID AAS32730 standard; DNA; 1515 BP.
 DE Human genomic DNA for novel endocrine antigen. SEQ ID No 684.
 PN WO200155319-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 4; Length 717;
 Best Local Similarity 82.4%; Pred. No. 5.2e-46;

RESULT 1120
 ID ABLS535 standard; cDNA; 2408 BP.
 DE Human protein synthesis initiation factor 10.12-encoding cDNA.
 PN CN1331221-A.

PD 16-JAN-2002.

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 Query Match 21.7%; Score 197; DB 6; Length 2408;
 Best Local Similarity 80.0%; Pred. No. 6.3e-46;

RESULT 1121
 ID ACC0229 standard; cDNA; 2969 BP.
 DE Breast cancer associated cDNA sequence SEQ ID NO:301.
 PN WO2003004989-A2.

PD 16-JUL-2003.

PA (MILL-) MILLENTUM PHARM INC.
 Query Match 21.7%; Score 197; DB 8; Length 2969;
 Best Local Similarity 82.5%; Pred. No. 6.8e-46;

RESULT 1122
 ID ADR07810 standard; cDNA; 3779 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 1316.
 PN EP147413-A2.

PD 18-AUG-2004.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 21.7%; Score 197; DB 13; Length 3779;
 Best Local Similarity 83.7%; Pred. No. 7.4e-46;

RESULT 1123
 ID ADP8449 standard; cDNA; 3834 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 1955.
 PN EP147413-A2.

PD 18-AUG-2004.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 21.7%; Score 197; DB 13; Length 3834;
 Best Local Similarity 78.9%; Pred. No. 7.5e-46;

RESULT 1124
 ID ADR07292 standard; cDNA; 3868 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 798.
 PN EP147413-A2.

PD 18-AUG-2004.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 21.7%; Score 197; DB 13; Length 3868;

Best Local Similarity 78.9%; Pred. No. 7.5e-46;

RESULT 1125
 ID AAK85025 standard; DNA; 5919 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39837.
 PN WO200157182-A2.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 4; Length 5919;
 Best Local Similarity 79.2%; Pred. No. 8.8e-46;

RESULT 1126
 ID AAZ5333 standard; DNA; 8396 BP.
 DE Human STP2 (phenol sulphotransferase 2) gene.
 PN WO9961630-A1.

PD 16-DEC-1999.

PA (AXIS-) AXIS PHARM INC.
 Query Match 21.7%; Score 197; DB 3; Length 8396;
 Best Local Similarity 74.2%; Pred. No. 1e-45;

RESULT 1127
 ID AAK8550 standard; DNA; 13246 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3126.
 PN WO20015314-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 4; Length 13246;
 Best Local Similarity 82.5%; Pred. No. 1.2e-45;

RESULT 1128
 ID AAK8551 standard; DNA; 13247 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3127.
 PN WO20015314-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 4; Length 13247;
 Best Local Similarity 82.5%; Pred. No. 1.2e-45;

RESULT 1129
 ID ABD2570 standard; DNA; 22047 BP.
 DE Human cancer-associated genomic DNA HD7-165.
 PN WO2004074220-A2.

PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 197; DB 13; Length 22047;
 Best Local Similarity 77.9%; Pred. No. 1.5e-45;

RESULT 1130
 ID ABD3137 standard; DNA; 22056 BP.
 DE Human cancer-associated (CA) gene HD7-016.
 PN WO2004058146-A2.

PD 15-JUL-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 197; DB 13; Length 22056;

Best Local Similarity 77.9%; Pred. No. 1.5e-45;
 RESULT 1131
 ID AAK81639 standard; DNA; 28011 BP.
 DR Human immune/baematopoietic antigen genomic sequence SEQ ID NO:36451.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 4; Length 28011;
 Best Local Similarity 82.4%; Pred. No. 1.6e-45;
 RESULT 1132
 ID ADC81584 standard; DNA; 28066 BP.
 DE Human GPCR gene SEQ ID NO:2037.
 PN EP1210724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 21.7%; Score 197; DB 10; Length 28066;
 Best Local Similarity 77.9%; Pred. No. 1.6e-45;
 RESULT 1133
 ID ARK90296 standard; DNA; 32199 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3872.
 PN WO200155310-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 4; Length 32199;
 Best Local Similarity 74.2%; Pred. No. 1.7e-45;
 RESULT 1134
 ID AAI57673 standard; DNA; 32199 BP.
 DE Human colorectal cancer antigen coding sequence SEQ ID NO: 210.
 PN WO200155350-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 4; Length 32199;
 Best Local Similarity 74.2%; Pred. No. 1.7e-45;
 RESULT 1135
 ID ABS99350 standard; DNA; 32199 BP.
 DE Genomic DNA #54 encoding human colorectal cancer related protein.
 PN US2003119349-A1.
 PD 29-AUG-2002.
 PA (ROSE-) ROSEN C A.
 PA (RUBE/-) RUBEN S M.
 PA (BARA-) BARASH S C.
 Query Match 21.7%; Score 197; DB 6; Length 32199;
 Best Local Similarity 74.2%; Pred. No. 1.7e-45;
 RESULT 1136
 ID ADB9303 standard; DNA; 32199 BP.
 DE Human colorectal cancer related polypeptide DNA #54.
 PN US2003054430-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 10; Length 32199;
 Best Local Similarity 74.2%; Pred. No. 1.7e-45;
 RESULT 1137
 ID ADQ59482 standard; DNA; 43709 BP.
 DE Human cancer-associated (CA) gene sequence SEQ ID NO:118.
 PN WO2004058288-A1.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 197; DB 12; Length 43709;
 Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 RESULT 1138
 ID ACM45130 standard; DNA; 61197 BP.
 DE Human genomic sequence hCG15017.
 PN WO2005073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY
 Best Local Similarity 79.5%; Score 197; DB 11; Length 61197;
 Best Local Similarity 77.3%; Pred. No. 2.2e-45;
 RESULT 1139
 ID ACM44082 standard; DNA; 71048 BP.
 DE Human genomic sequence hCG39199.
 PN WO2003073826-A2.
 PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY
 Query Match 21.7%; Score 197; DB 11; Length 71048;
 Best Local Similarity 83.7%; Pred. No. 2.3e-45;
 RESULT 1140
 PA (SAGR-) SAGRES DISCOVERY
 Best Local Similarity 78.4%; Pred. No. 2.7e-45;
 Best Local Similarity 78.4%; Pred. No. 2.7e-45;
 RESULT 1141
 ID ACN4442 standard; DNA; 114931 BP.
 DE Human genomic sequence hCG27894.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY
 Query Match 21.7%; Score 197; DB 11; Length 114931;
 Best Local Similarity 80.0%; Pred. No. 2.8e-45;
 RESULT 1142
 ID ARV52850 standard; DNA; 116624 BP.
 DE Human eyal gene contig 4405-9480.
 PN WO9822849-A2.
 PD 30-JUL-1998.
 PA (INSP) INST PASTEUR
 Query Match 21.7%; Score 197; DB 2; Length 116624;
 Best Local Similarity 80.0%; Pred. No. 2.8e-45;
 RESULT 1143
 ID ACN44574 standard; DNA; 116792 BP.
 DE Human genomic sequence hCG18576.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY
 Query Match 21.7%; Score 197; DB 11; Length 116792;
 Best Local Similarity 79.2%; Pred. No. 2.8e-45;
 RESULT 1144
 ID ADI20995 standard; DNA; 119501 BP.
 DE Human MARK genomic DNA.
 PN WO2003232771-A1.
 PD 18-DEC-2003.
 PA (ISIS-) ISIS PHARM INC
 Query Match 21.7%; Score 197; DB 12; Length 119501;
 Best Local Similarity 79.8%; Pred. No. 2.8e-45;
 RESULT 1145
 ID ADB5096 standard; DNA; 119596 BP.
 DE Human G-protein coupled receptor gene.
 PA (SAGR-) SAGRES DISCOVERY
 Query Match 21.7%; Score 197; DB 6; Length 119596;
 Best Local Similarity 77.3%; Pred. No. 2.8e-45;
 RESULT 1146
 ID ADE4382 standard; DNA; 128034 BP.
 DE Polymorphic human IDE genomic sequence, SEQ ID 187.
 PN WO200305413-A2.
 PD 03-JUL-2003.
 PA (NEUR-) NEUROGENETICS INC.
 PA (GEHO) GEN HOSPITAL CORP.
 Query Match 21.7%; Score 197; DB 10; Length 128034;
 Best Local Similarity 80.0%; Pred. No. 2.9e-45;
 RESULT 1147
 ID ADB43581 standard; DNA; 128034 BP.
 DE Human IDE genomic sequence, SEQ ID 186.
 PN WO200305413-A2.
 PD 03-JUL-2003.
 PA (NEUR-) NEUROGENETICS INC.
 PA (GEHO) GEN HOSPITAL CORP.
 Query Match 21.7%; Score 197; DB 10; length 128034;
 Best Local Similarity 80.0%; Pred. No. 2.9e-45;
 RESULT 1148
 ID ADH54059 standard; DNA; 128034 BP.
 DE Human IDE gene DNA sequence SeqID186.
 PN US2003224380-A1.
 PD 04-DEC-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 Query Match 21.7%; Score 197; DB 12; Length 128034;
 Best Local Similarity 80.0%; Pred. No. 2.9e-45;
 RESULT 1149
 ID ADH54060 standard; DNA; 128034 BP.
 DE Human IDE gene variant DNA sequence SeqID187.
 PN US2003224380-A1.

PD 04-DEC-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 Query Match 21.7%; Score 197; DB 12; Length 128034;
 Best Local Similarity 80.0%; Pred. No. 2.9e-45;
 RESULT 1150
 ID ABN8735 Standard; DNA; 155074 BP.
 DE Human genomic region containing the ltrpc5 gene SEQ ID NO 6.
 PN WO2002540659-A1.
 PD 11-JUL-2002.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 21.7%; Score 197; DB 6; Length 155074;
 Best Local Similarity 81.1%; Pred. No. 3.1e-45;
 RESULT 1151
 ID ADQ20461 standard; DNA; 16181 BP.
 DR Human soft tissue sarcoma-upregulated DNA - SEQ ID 3281.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 ID ADQ18633 Standard; DNA; 166181 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1452.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 21.7%; Score 197; DB 12; Length 166181;
 Best Local Similarity 82.5%; Pred. No. 3.2e-45;
 RESULT 1152
 ID ADQ18633 Standard; DNA; 166181 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1452.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 197; DB 11; Length 174448;
 Best Local Similarity 78.9%; Pred. No. 3.3e-45;
 RESULT 1154
 ID DE Outbearthritis-associated polymorphic nucleotide #467.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 21.7%; Score 197; DB 10; Length 177866;
 Best Local Similarity 84.0%; Pred. No. 3.3e-45;
 RESULT 1155
 ID ACM4459 Standard; DNA; 21231 BP.
 DE Human genomic sequence hcg401221.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 197; DB 11; Length 212231;
 Best Local Similarity 77.1%; Pred. No. 3.5e-45;
 RESULT 1156
 ID ACM44194 Standard; DNA; 275449 BP.
 DE Human genomic sequence hcg23995.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 197; DB 11; Length 275449;
 Best Local Similarity 80.0%; Pred. No. 3.9e-45;
 RESULT 1157
 ID ADB6528 Standard; cDNA; 2308 BP.
 DE Human cDNA encoding clone HHDRP220082790.
 PN EP1308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.
 Query Match 21.7%; Score 197; DB 11; Length 275449;
 Best Local Similarity 80.0%; Pred. No. 3.9e-45;
 RESULT 1158
 ID ADQ8639 Standard; cDNA; 2320 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #3714.
 PN WO2004060270-A2.
 PD 10-JUN-2004.

PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD-) WU T D.
 PA (ZHOU/) ZHOU Y.
 Query Match 21.7%; Score 196.8; DB 12; Length 2320;
 Best Local Similarity 80.5%; Pred. No. 7e-46;
 RESULT 1159
 ID ADQ8620 Standard; cDNA; 2320 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #434.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD-) WU T D.
 PA (ZHOU/) ZHOU Y.
 Query Match 21.7%; Score 196.8; DB 13; Length 2320;
 Best Local Similarity 80.5%; Pred. No. 7e-46;
 RESULT 1160
 ID ADQ8624 Standard; cDNA; 2320 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #1108.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD-) WU T D.
 PA (ZHOU/) ZHOU Y.
 Query Match 21.7%; Score 196.8; DB 13; Length 2320;
 Best Local Similarity 80.5%; Pred. No. 7e-46;
 RESULT 1161
 ID ADQ8604 Standard; cDNA; 2320 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #858.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD-) WU T D.
 PA (ZHOU/) ZHOU Y.
 Query Match 21.7%; Score 196.8; DB 13; Length 2320;
 Best Local Similarity 80.5%; Pred. No. 7e-46;
 RESULT 1162
 ID DE Tumour-associated antigenic target (TAT) cDNA DNA326665, SEQ ID NO:5419.
 PN WO200403015-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.8; DB 13; Length 2320;
 Best Local Similarity 80.5%; Pred. No. 7e-46;
 RESULT 1163
 ID ADM02495 Standard; cDNA; 2404 BP.
 DE Human cDNA of the invention SEQ ID NO:1180.
 PN EP1347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RSS ASSOC BIOTECHNOLOGY.
 Query Match 21.7%; Score 196.8; DB 11; Length 2404;
 Best Local Similarity 78.5%; Pred. No. 7.1e-46;
 RESULT 1164
 ID ABQ8160 Standard; cDNA; 2631 BP.
 DE Human fumurate reductase/succinic dehydrogenase 9.13 cDNA SEQ ID NO:1.
 PN CN1345948-A.
 PD 24-APR-2002.
 PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 Query Match 21.7%; Score 196.8; DB 6; Length 2631;
 Best Local Similarity 84.7%; Pred. No. 7.4e-46;
 RESULT 1165
 ID AAK674 Standard; DNA; 5079 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21556.
 PN WO20015782-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 4; Length 5079;
 Best Local Similarity 79.5%; Pred. No. 9.5e-46;
 RESULT 1166
 ID ADQ24919 Standard; DNA; 6833 BP.
 DE Human soft tissue barcoma-upregulated DNA - SEQ ID 7739.
 PN WO2004048938-A2.
 PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC. Query Match 21.7%; Score 196.8; DB 12; Length 6833; Best Local Similarity 84.7%; Pred. No. 1.1e-45; RESULT 1167

ID ADQ2145 Standard; DNA; 6833 BP.

DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6965.

FN WO2004048938-A2.

PD 02-AUG-2004.

PA (PROT-) PROTEIN DESIGN LABS INC. Query Match 21.7%; Score 196.8; DB 12; Length 6833; Best Local Similarity 84.7%; Pred. No. 1.1e-45; RESULT 1168

ID AAI62666 Standard; DNA; 7444 BP.

DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 316.

PN WO200155324-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.8; DB 4; Length 7444; Best Local Similarity 83.4%; Pred. No. 1.1e-45; RESULT 1169

ID AAL06760 Standard; DNA; 7444 BP.

DE Human reproductive system related antigen DNA SEQ ID NO: 9448.

PN WO200155320-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.8; DB 4; Length 7444; Best Local Similarity 83.4%; Pred. No. 1.1e-45; RESULT 1170

ID AAL06118 Standard; DNA; 7444 BP.

DE Human reproductive system related antigen DNA SEQ ID NO: 8806.

PN WO200155320-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.8; DB 4; Length 7444; Best Local Similarity 83.4%; Pred. No. 1.1e-45; RESULT 1171

ID ABL9863 standard; DNA; 7444 BP.

DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3335.

PN WO200155311-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.8; DB 4; Length 7444; Best Local Similarity 83.4%; Pred. No. 1.1e-45; RESULT 1172

ID ABL15867 Standard; DNA; 7444 BP.

DE Human nervous system related polynucleotide SEQ ID NO 8198.

PN WO200159063-A2.

PD 16-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.8; DB 5; Length 7444; Best Local Similarity 83.4%; Pred. No. 1.1e-45; RESULT 1173

ID AAK66749 Standard; DNA; 9324 BP.

DE Human immune-haematopoietic antigen genomic sequence SEQ ID NO:21561.

PN WO200157182-A2.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.8; DB 4; Length 9324; Best Local Similarity 79.5%; Pred. No. 1.2e-45; RESULT 1174

ID AAS2895 Standard; DNA; 9765 BP.

DE Human immunoglobulin encoding genomic DNA SEQ ID NO 257.

PN WO20015315-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.8; DB 4; Length 9765; Best Local Similarity 78.0%; Pred. No. 1.2e-45; RESULT 1175

ID AAS2886 Standard; DNA; 9765 BP.

DE Human immunoglobulin encoding genomic DNA SEQ ID NO 248.

PN WO20015315-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.8; DB 4; Length 9765; Best Local Similarity 78.0%; Pred. No. 1.2e-45; RESULT 1176

ID ABA05802 Standard; DNA; 9765 BP.

DE Human genomic DNA SEQ ID NO: 888.

PN WO200154474-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.8; DB 4; Length 9765; Best Local Similarity 78.0%; Pred. No. 1.2e-45; RESULT 1177

ID ABA0649 Standard; DNA; 9765 BP.

DE Human genomic DNA SEQ ID NO: 935.

PN WO200154474-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.8; DB 4; Length 9765; Best Local Similarity 78.0%; Pred. No. 1.2e-45; RESULT 1178

ID ABB84139 Standard; DNA; 9765 BP.

DE Human polynucleotide SEQ ID NO 888.

PN US20020190672-A1.

PD 11-JUL-2002.

PA (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.

PA (BARA/) RUBEN S M.

PA (BARA/) BARASH S C.

Query Match 21.7%; Score 196.8; DB 6; Length 9765; Best Local Similarity 78.0%; Pred. No. 1.2e-45; RESULT 1179

ID ABV84186 Standard; DNA; 9765 BP.

DE Human polynucleotide SEQ ID NO 935.

PN US20020190672-A1.

PD 11-JUL-2002.

PA (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.

Query Match 21.7%; Score 196.8; DB 6; Length 9765; Best Local Similarity 78.0%; Pred. No. 1.2e-45; RESULT 1180

ID ADB31736 Standard; DNA; 9765 BP.

DE Human novel protein DNA SEQ ID NO 257.

PN US20030377606-A1.

PD 24-APR-2003.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.8; DB 10; Length 9765; Best Local Similarity 78.0%; Pred. No. 1.2e-45; RESULT 1181

ID ADB31727 Standard; DNA; 9765 BP.

DE Human novel protein DNA SEQ ID NO 248.

PN US20030377606-A1.

PD 24-APR-2003.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.8; DB 10; Length 9765; Best Local Similarity 78.0%; Pred. No. 1.2e-45; RESULT 1182

ID AAS42100 Standard; DNA; 12295 BP.

DE Genomic sequence #416 encoding novel human enzyme polypeptide.

PN WO20015315-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.8; DB 4; Length 12595; Best Local Similarity 80.5%; Pred. No. 1.4e-45; RESULT 1183

ID ABA15617 Standard; DNA; 1586 BP.

DE Human nervous system related polynucleotide SEQ ID NO 7948.

PN WO200150063-A2.

PD 16-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.8; DB 4; Length 15186; Best Local Similarity 82.0%; Pred. No. 1.5e-45; RESULT 1184

ID ABA15616 Standard; DNA; 15187 BP.

DE Human nervous system related polynucleotide SEQ ID NO 7947.

- PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 5; Length 15187;
 Best Local Similarity 82.0%; Pred. No. 1.5e-45;
 RESULT 1185
 ID AAK86680 Standard; DNA; 17357 BP.
 DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:41492.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 83.2%; Pred. No. 1.5e-45;
 RESULT 1186
 ID AAK86681 Standard; DNA; 17363 BP.
 DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:41493.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 83.2%; Pred. No. 1.5e-45;
 RESULT 1187
 ID ADC85168 Standard; DNA; 21704 BP.
 DE Human GCR gene SEQ ID NO:621.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED SCI & TECHNOLOGY INCUBATIO.
 (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match Best Local Similarity 21.7%; Score 196.8; DB 4; Length 17363;
 Best Local Similarity 79.5%; Pred. No. 1.5e-45;
 RESULT 1188
 ID ADQ91776 Standard; DNA; 25694 BP.
 DE Human cancer associated sequence HD10-045, SEQ ID 753.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match Best Local Similarity 79.5%; Pred. No. 1.7e-45;
 Best Local Similarity 79.5%; Pred. No. 1.7e-45;
 RESULT 1189
 ID AB552813 Standard; DNA; 27847 BP.
 DE Genomic DNA encoding human secreted protein #1.
 PN WO200264626-A2.
 PD 22-AUG-2002.
 PA (PEKE) PE CORP NY.
 Query Match Best Local Similarity 81.8%; Pred. No. 1.8e-45;
 Best Local Similarity 81.8%; Pred. No. 1.8e-45;
 RESULT 1190
 ID AD97189 standard; DNA; 29360 BP.
 DE Human cancer associated sequence HD08-012, SEQ ID 165.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match Best Local Similarity 80.7%; Pred. No. 1.9e-45;
 Best Local Similarity 80.7%; Pred. No. 1.9e-45;
 RESULT 1191
 ID ALM37292 Standard; DNA; 32192 BP.
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 3657.
 PN WO200155367-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 RESULT 1192
 ID ALM07103 Standard; DNA; 32192 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9791.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 RESULT 1193
 ID ABX0280 Standard; cDNA; 32192 BP.
 DE cDNA encoding novel human musculoskeletal system antigen #2624.
-
- PN US2002147140-A1.
 PD 10-OCT-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 RESULT 1194
 ID ADJ31030 Standard; DNA; 32192 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3657.
 PN US200409488-A1.
 PD 15-JUN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 RESULT 1195
 ID ABL6428 Standard; DNA; 35641 BP.
 DE Stomach cancer related gene sequence SEQ ID NO:2765.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match Best Local Similarity 82.0%; Pred. No. 2e-45;
 Best Local Similarity 82.0%; Pred. No. 2e-45;
 RESULT 1196
 ID ABN95727 Standard; DNA; 35641 BP.
 DE Gene #2225 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENIE LOGIC INC.
 Query Match Best Local Similarity 82.0%; Pred. No. 2e-45;
 Best Local Similarity 82.0%; Pred. No. 2e-45;
 RESULT 1197
 ID AAK7372 Standard; DNA; 37925 BP.
 DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:27184.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match Best Local Similarity 79.5%; Pred. No. 2.1e-45;
 Best Local Similarity 79.5%; Pred. No. 2.1e-45;
 RESULT 1198
 ID ADJ12847 Standard; DNA; 37925 BP.
 DE DNA fragment of a BAC clone that encodes a human secreted protein Seq701.
 PN US2004010132-A1.
 PD 15-JAN-2004.
 PA (ROSE/) ROSEN C A.
 PA (BREW/) BREWER L A.
 PA (DUAN/) DUAN R D.
 PA (RUBE/) RUBEN S M.
 PA (FLOR/) FLORENCE K A.
 PA (GREE/) GREENE J M.
 PA (YOUN/) YOUNG P E.
 PA (FERR/) FERRE A M.
 PA (YUGG/) YU G.
 PA (FLOR/) FLORENCE C.
 PA (EBNE/) EBNER R.
 PA (OLSE/) OLSEN H.
 Query Match Best Local Similarity 79.5%; Pred. No. 2.1e-45;
 Best Local Similarity 79.5%; Pred. No. 2.1e-45;
 RESULT 1199
 ID ABK8508 Standard; DNA; 43545 BP.
 DE Human cathein-like asymmetry protein-2 (CLASP-2) genomic DNA.
 PN WO200231177-A2.
 PD 18-APR-2002.
 PA (ARBO-) ARBOR VITA CORP.
 PA (GARM/) GARMAN J D.
 PA (CAND/) CANDIA A F.
 Query Match Best Local Similarity 76.9%; Pred. No. 2.2e-45;
 Best Local Similarity 76.9%; Pred. No. 2.2e-45;
 RESULT 1200
 ID ADA02960 Standard; DNA; 44325 BP.
 DE Human DADI carcinoma associated gene, SEQ ID NO:1478.
 PN WO2003057146-A2.
 PD 17-JUL-2003.

PA (SAGR-) SAGRES DISCOVERY 21.7%; Score 196.8; DB 9; Length 44325;
 DE Human PLZF DNA corresponding to AF060568.
 Best Local Similarity 82.0%; Pred. No. 2.2e-45;
 RESULT 1201
 ID ADB77698 standard; DNA; 44325 BP.
 DE Human DADI gene.
 PN WO200308583-A2.
 PA (SAGR-) SAGRES DISCOVERY 21.7%; Score 196.8; DB 10; Length 44325;
 Best Local Similarity 82.0%; Pred. No. 2.2e-45;
 RESULT 1202
 ID ADC8540 standard; DNA; 44325 BP.
 DE Human Dadi genomic sequence.
 PN WO2003045203-A2.
 PD 05-JUN-2003.
 PA (SAGR-) SAGRES DISCOVERY 21.7%; Score 196.8; DB 10; Length 44325;
 Best Local Similarity 82.0%; Pred. No. 2.2e-45;
 RESULT 1203
 ID ADM74555 standard; DNA; 44325 BP.
 DE Human carcinoma associated (CA) nucleic acid #112.
 PN US2004072154-A1.
 PD 15-APR-2004.
 PA (MORR-) MORRIS D W.
 Query Match ENGBERHARD E K.
 Best Local Similarity 82.0%; Score 196.8; DB 12; Length 44325;
 RESULT 1204
 ID ABD32574 standard; DNA; 43944 BP.
 DE Human cancer-associated genomic DNA HD7-204.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.8; DB 13; Length 45944;
 Best Local Similarity 81.8%; Pred. No. 2.2e-45;
 RESULT 1205
 ID AAD42934 standard; DNA; 70000 BP.
 DE Human phospholipase A2 (PLA2), group VI (Ca2+-independent) gene.
 PN US6140325-B1.
 PD 25-JUN-2002.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.7%; Score 196.8; DB 6; Length 70000;
 Best Local Similarity 79.5%; Pred. No. 2.6e-45;
 RESULT 1206
 ID ADB0875 standard; DNA; 461 BP.
 DE Human ovarian carcinoma antigen polynucleotide #1.
 PN WO200306317-A2.
 PD 24-JAN-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 21.7%; Score 196.6; DB 6; Length 461;
 Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1214
 ID ABN7258 standard; DNA; 461 BP.
 DE Ovarian carcinoma antigen polynucleotide #3.
 PN WO200306317-A2.
 PD 15-MAY-2003.
 PA (MITC-) MITCHAM J L.
 Query Match 21.7%; Score 196.8; DB 12; Length 87411;
 Best Local Similarity 79.1%; Pred. No. 2.8e-45;
 RESULT 1207
 ID ABD3342 standard; DNA; 106938 BP.
 DE Human cancer-associated (CA) gene HD07-081.
 PN WO200405816-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.8; DB 13; Length 106938;
 Best Local Similarity 81.8%; Pred. No. 3.1e-45;
 RESULT 1208
 ID ADR67034 standard; DNA; 106938 BP.
 DE Human cancer associated gene genomic sequence SEQ ID NO:80.
 PN WO2004074321-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.8; DB 13; Length 106938;
 Best Local Similarity 81.8%; Pred. No. 3.1e-45;
 RESULT 1209
 ID ADL17884 standard; cDNA; 158001 BP.
 DE Human phosphotyrosyl phosphatase activator, PTPA, gene.
 PN US2004023906-A1.
 PD 05-FEB-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.7%; Score 196.8; DB 12; Length 158001;
 Best Local Similarity 84.5%; Pred. No. 3.6e-45;
 RESULT 1210
 ID ACM64924 standard; DNA; 201239 BP.

Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1217
 ID ADP08499 Standard; cDNA; 461 BP.
 DE cDNA encoding Secreted ovarian carcinoma antigen Seqid 3.
 PN US2003124140-A1.
 PD 03-JUL-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 21.7%; Score 196.6; DB 10; Length 461;
 Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1218
 ID ADP08497 standard; cDNA; 461 BP.
 DE cDNA encoding secreted ovarian carcinoma antigen seqid 1.
 PN US2003124140-A1.
 PD 03-JUL-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 21.7%; Score 196.6; DB 10; Length 461;
 Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1219
 ID ADG46347 Standard; cDNA; 461 BP.
 DE Human ovarian carcinoma polynucleotide #3.
 PN US2003165504-A1.
 PD 04-SEP-2003.
 PA (RETT-) RETTER M W.
 (PANG-) RANGER G R.
 Query Match 21.7%; Score 196.6; DB 10; Length 461;
 Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1220
 ID ADG46345 Standard; cDNA; 461 BP.
 DE Human ovarian carcinoma polynucleotide #1.
 PN US2003165504-A1.
 PD 04-SEP-2003.
 PA (RETT-) RETTER M W.
 (PANG-) RANGER G R.
 Query Match 21.7%; Score 196.6; DB 10; Length 461;
 Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1221
 ID AAK15355 Standard; cDNA; 1652 BP.
 DE Human cDNA sequence SEQ ID NO:13531.
 PN EP104617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 21.7%; Score 196.6; DB 4; Length 1652;
 Best Local Similarity 80.2%; Pred. No. 7.1e-46;
 RESULT 1222
 ID AS21268 Standard; cDNA; 3719 BP.
 DE Human cDNA sequence encoding for PRO4799 polypeptide.
 PN WO200140466-A2.
 PD 07-JUN-2001.
 PA (GETH-) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 4; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 7.1e-46;
 RESULT 1223
 ID ACA03627 Standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH-) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 4; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1224
 ID ABX69165 standard; cDNA; 3719 BP.
 DE DNA encoding novel secreted and transmembrane protein PRO4799.
 PN US200317563-A1.
 PD 23-JAN-2003.
 PA (GETH-) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 8; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1225
 ID AC041819 Standard; cDNA; 3719 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #25.
 PN US2003036179-A1.
 PD 22-FEB-2003.
 PA (GETH-) GENENTECH INC.

Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1226
 ID ACA04048 Standard; cDNA; 3719 BP.
 DE Human cDNA encoding a Secreted/transmembrane protein, SEQ ID 49.
 PN US2003032155-A1.
 PD 13-FEB-2003.
 PA (GETH-) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 8; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1227
 ID ADA5568 Standard; cDNA; 3719 BP.
 DE Novel human Secreted and transmembrane protein PRO4799 cDNA.
 PN US200302228-A1.
 PD 30-JAN-2003.
 PA (GETH-) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1228
 ID ADA75999 Standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003073212-A1.
 PD 17-APR-2003.
 PA (GETH-) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1229
 ID ADA18649 Standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003054517-A1.
 PD 20-MAR-2003.
 PA (GETH-) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1230
 ID ADA61272 Standard; cDNA; 3719 BP.
 DE Homo Sapiens.
 PN US2003049816-A1.
 PD 13-MAR-2003.
 PA (GETH-) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1231
 ID ADB11057 Standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003068796-A1.
 PD 10-APR-2003.
 PA (GETH-) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1232
 ID ADB27598 Standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003082704-A1.
 PD 01-MAY-2003.
 PA (GETH-) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1233
 ID ADA88077 Standard; cDNA; 3719 BP.
 DE Novel human Secreted and transmembrane protein PRO4799 cDNA.
 PN US2003082711-A1.
 PD 01-MAY-2003.
 PA (GETH-) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1234
 ID ADB15641 Standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003087350-A1.
 PD 08-MAY-2003.
 PA (GETH-) GENENTECH INC.

Query Match 21.7%; Score 196.6; DB 9; Length 3719;

Best Local Similarity 80.2%; Pred. No. 9.6e-46; RESULT 1235
ID ADA47427 standard; cDNA: 3719 BP.
DE Human PRO poly nucleotide #25.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1236
ID ADA6722 standard; cDNA: 3719 BP.
DE Human PRO poly nucleotide #25.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1237
ID ADB3029 standard; cDNA: 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1238
ID ADA8525 standard; cDNA: 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082633-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1239
ID ADA96737 standard; cDNA: 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1240
ID ADR75041 standard; cDNA: 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1241
ID ADR87180 standard; cDNA: 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1242
ID ADR16382 standard; cDNA: 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1243
ID ADR91474 standard; cDNA: 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1244
ID ADR9313 standard; cDNA: 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1245
ID ADB18498 standard; cDNA: 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1246
ID ADR9313 standard; cDNA: 3719 BP.
DE Human PRO poly nucleotide #25.
PN US2003077722-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1247
ID ADB18609 standard; cDNA: 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1248
ID ADB1221 standard; cDNA: 3719 BP.
DE Human PRO poly nucleotide #25.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1249
ID ACD9848 standard; cDNA: 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1250
ID ADR74175 standard; cDNA: 3719 BP.
DE Human PRO poly nucleotide #25.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1251
ID ADB24408 standard; cDNA: 3719 BP.
DE Human PRO poly nucleotide SEQ ID NO 49.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1252
ID ADR81932 standard; cDNA: 3719 BP.
DE Human PRO poly nucleotide #25.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1253

ID ADA74895 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003073246-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1254
ID ADA84973 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1255
ID ADA84421 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1256
ID ADB29677 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003073214-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1257
ID ADA80205 standard; cDNA; 3719 BP.
DE Human PRO Polynucleotide #25.
PN US2003082761-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1258
ID ADA75447 standard; cDNA; 3719 BP.
DE Human PRO Polynucleotide #25.
PN US2003082703-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1259
ID ADA46672 standard; cDNA; 3719 BP.
DE Human PRO Polynucleotide #25.
PN US2003073210-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1260
ID ADB2968 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide SEQ ID NO 49.
PN US2003077715-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1261
ID ADA93144 standard; cDNA; 3719 BP.
DE Human PRO Polynucleotide #25.
PN US2003077721-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1262
ID ADB26494 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1263
ID ADB30781 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO Polypeptide #25.
PN US2003096386-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1264
ID ADA60709 standard; cDNA; 3719 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1265
ID ADB2885 standard; cDNA; 3719 BP.
DE Human PRO Polynucleotide SEQ ID NO 49.
PN US2003077114-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1266
ID ADA96185 standard; cDNA; 3719 BP.
DE Human PRO Polynucleotide #25.
PN US2003082930-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1267
ID ADA8077 standard; cDNA; 3719 BP.
DE Human PRO Polynucleotide #25.
PN US2003082702-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1268
ID ADA95633 standard; cDNA; 3719 BP.
DE Human PRO Polynucleotide #25.
PN US2003082159-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1269
ID ADB25942 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003082760-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1270
ID ADB21427 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1271
ID ADA77206 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.

PN US2003068797-A1.
 PD 01-APR-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 9; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1272
 ID ADB17946 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003077710-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 9; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1273
 ID ADA8629 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003082709-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 9; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1274
 ID ADR87132 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003082700-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 9; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1275
 ID ADA46120 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003054516-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 9; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1276
 ID ADB28150 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003082699-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 9; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1277
 ID ADB28702 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003082706-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 9; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1278
 ID ADB7654 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003059905-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 9; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1279
 ID ADR88284 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003073213-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 9; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1280
 ID ADR97289 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003082686-A1.

Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1290
 ID ADB6261 Standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003082689-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1291
 ID ADB8341 Standard; cDNA; 3719 BP.
 DE Human PRO Polynucleotide #25.
 PN US2003082698-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1292
 ID ADB9073 Standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003082762-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1293
 ID ADB9174 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003082764-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1294
 ID ADC4697 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003082766-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1295
 ID ADB8640 Standard; cDNA; 3719 BP.
 DE Human PRO Polynucleotide #25.
 PN US2003082867-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1296
 ID ADB7709 Standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003082869-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1297
 ID ADB3166 Standard; cDNA; 3719 BP.
 DE Human PRO Polynucleotide SEQ ID NO 49.
 PN US2003082866-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1298
 ID ADB5270 Standard; cDNA; 3719 BP.
 DE Human PRO Polynucleotide SEQ ID NO 49.
 PN US2003077719-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1299
 ID ADC3614 Standard; cDNA; 3719 BP.
 DE Human PRO Polynucleotide SEQ ID NO 49.
 PN US2003077716-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1300
 ID ADB3718 Standard; cDNA; 3719 BP.
 DE Human PRO Polynucleotide SEQ ID NO 49.
 PN US2003077718-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1301
 ID ADB5822 Standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide SEQ ID NO 49.
 PN US2003077720-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1302
 ID ADC46217 Standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003082892-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1303
 ID ADC5090 Standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003092106-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1304
 ID ADC71637 Standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003092107-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1305
 ID ADC59616 Standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003092105-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1306
 ID ADC2623 Standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID49.
 PN US2003087365-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1307
 ID ADC56977 Standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID49.
 PN US2003087366-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1308

ID ADC60168 standard; cDNA; 3719 BP.
 DB Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087367-A1.

PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1309
 ID ADC50643 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087361-A1.

PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1310
 ID ADC65170 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003087352-A1.

PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1311
 ID ADC54268 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID49.
 PN US2003087363-A1.

PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1312
 ID ADC53229 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID49.
 PN US2003087364-A1.

PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1313
 ID ADC58752 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087359-A1.

PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1314
 ID ADC55630 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID49.
 PN US2003087360-A1.

PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1315
 ID ADC58200 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087346-A1.

PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1316
 ID ADD02874 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003092104-A1.

PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1317
 ID ADC9866 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1326
 ID ADD09151 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.

PN US2003194775-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Query Match
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1327
 ID ADD40864 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003203438-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1328
 ID ADD5003 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003194769-A1.
 PD 15-OCT-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1329
 ID ADD5243 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003194752-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1330
 ID ADD5295 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003194747-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1331
 ID ADD5451 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003194779-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1332
 ID ADD0250 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003194731-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1333
 ID ADD01684 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003194732-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1334
 ID ADD5866 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003194732-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1343
 ID ADD91631 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003194732-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1344
 ID ADE33094 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003194767-A1.
 PD 16-OCT-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1345
 ID ADE3146 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003114791-A1.
 PD 16-OCT-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1346
 ID ADD7969 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003207417-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1347
 ID ADD9275 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003194768-A1.
 PD 16-OCT-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1348
 ID ADE19155 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003199031-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1349
 ID ADE1803 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003199036-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1350
 ID ADE42799 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003199033-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1350
 ID ADE42799 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003199033-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1351
 ID ADD9588 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003199035-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1352
 ID ADE22474 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003199064-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1353
 ID ADD78592 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003103429-A1.
 PD 16-OCT-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1361
 ID ADD21199 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207353-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1362
 ID ADD22810 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003070784-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1363
 ID ADP9715 standard; cDNA; 3719 BP.
 DE Human PRO Polynucleotide #25.
 PN US2003207370-A1.
 PD 05-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1364
 ID ADG80239 standard; cDNA; 3719 BP.
 DE Human PRO Polynucleotide #25.
 PN US2003207373-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1365
 ID ADG9687 standard; cDNA; 3719 BP.
 DE Human PRO Polynucleotide #25.
 PN US2003207372-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1366
 ID ADH4979 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207381-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1367
 ID ADH5531 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207379-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1368
 ID ADI63750 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207385-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1369
 ID ADI64699 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207386-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1370
 ID ADI63198 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207387-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1371
 ID ADH31612 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207388-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1372
 ID ADH81060 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207377-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1373
 ID ACD2877 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003321556-A1.
 PD 13-FEB-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1374
 ID ACA67018 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US200300311-A1.
 PD 02-JAN-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1375
 ID ADM8229 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087355-A1.
 PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1376
 ID ADM15628 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087353-A1.
 PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1377
 ID ADN16257 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087355-A1.
 PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1378
 ID ADN15076 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087356-A1.
 PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1379
 ID ADN14524 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087357-A1.
 PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1380
 ID ADC80786 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003092115-A1.
 PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match Similarity 80.2%; Pred. No. 9.6e-46;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1381

ID ADD76234 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003100887-A1.
 PD 29-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1382

ID ADD87598 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003092113-A1.
 PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1383

ID ADD86002 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003092340-A1.
 PD 30-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1384

ID ADE75450 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US200311571-A1.
 PD 13-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1385

ID ADE23026 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003092108-A1.
 PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1386

ID ADE23578 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003092110-A1.
 PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1387

ID ADE24221 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003092111-A1.
 PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1388

ID ADB87046 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003203439-A1.
 PD 30-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1389

ID ADE88912 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003203439-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1390

ID ADB18051 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003199062-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1391

ID ADB83360 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003199054-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1392

ID ADE94180 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003199057-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1393

ID ADE0191 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003199051-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1394

ID ADE94932 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003199052-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1395

ID ADE93012 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003199050-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1396

ID AUF3463 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003199029-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1397

ID AUF3463 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003199051-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1398

ID AUF90239 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003199053-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1399

ID AUF9198 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003199055-A1.

PN US2003199058-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1401
 ID ADG01965 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003207352-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1401
 ID ADG21751 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207360-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1402
 ID ADG19821 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003207376-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1403
 ID ADG9777 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003207422-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1404
 ID ADG23944 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207426-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1405
 ID ADG90298 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003208055-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1406
 ID ADG03129 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003207351-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1407
 ID ADG98850 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003207353-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1408
 ID ADG16435 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003207359-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1409
 ID ADG04894 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003207375-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1410
 ID ADG19161 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003207425-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1411
 ID ADG12998 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003207357-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1412
 ID ADG0055 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207424-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1413
 ID ADG15225 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003219895-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1414
 ID ADG96623 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003207371-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1415
 ID ADG05808 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003207374-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1416
 ID ADG23392 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207389-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1417
 ID ADG03681 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003207423-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1427
 ID ADG5478 Standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207427-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1419
 ID ADG6879 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207350-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1420
 ID ADG0431 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207356-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1421
 ID ADG5426 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207356-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1422
 ID ADG6090 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207350-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1423
 ID ADG61694 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207428-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1424
 ID ADG81895 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003207358-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1425
 ID ADG57134 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207362-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1426
 ID ADG56582 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207364-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Query Match Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1436
ID ADG52094 standard; cDNA: 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 21.7%; Score 196.6; DB 12; Length 3719;
Pred. No. 9.6e-46;

RESULT 1437
ID ADG5822 standard; cDNA: 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 21.7%; Score 196.6; DB 12; Length 3719;
Pred. No. 9.6e-46;

RESULT 1438
ID ADG60791 standard; cDNA: 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003194793-A1.
PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 21.7%; Score 196.6; DB 12; Length 3719;
Pred. No. 9.6e-46;

RESULT 1439
ID ADG5030 standard; cDNA: 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207366-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 21.7%; Score 196.6; DB 12; Length 3719;
Pred. No. 9.6e-46;

RESULT 1440
ID ADH12296 standard; cDNA: 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 21.7%; Score 196.6; DB 12; Length 3719;
Pred. No. 9.6e-46;

RESULT 1441
ID ADG6142 standard; cDNA: 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 21.7%; Score 196.6; DB 12; Length 3719;
Pred. No. 9.6e-46;

RESULT 1442
ID ADH20229 standard; cDNA: 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003202331-A1.
PD 30-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 21.7%; Score 196.6; DB 12; Length 3719;
Pred. No. 9.6e-46;

RESULT 1443
ID ADG53374 standard; cDNA: 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 21.7%; Score 196.6; DB 12; Length 3719;
Pred. No. 9.6e-46;

RESULT 1444
ID ADG9414 standard; cDNA: 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 21.7%; Score 196.6; DB 12; Length 3719;
Pred. No. 9.6e-46;

RESULT 1445
ID ADG53374 standard; cDNA: 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 21.7%; Score 196.6; DB 12; Length 3719;
Pred. No. 9.6e-46;

RESULT 1445
ID ADM27413 standard; cDNA: 3719 BP.

DE cDNA encoding human PRO polypeptide #25.
 PN US2004048333-A1.
 PD 11-MAR-2004.
 PA (GETH-) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1455 ID ADM1937 standard; cDNA; 3719 BP.
 DE PRO4977 encoding sequence.
 PN WO2004024077-A2.
 PD 25-MAR-2004.
 PA (GETH-) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1456 ID ADM42137 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2004058424-A1.
 PA (GETH-) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1457 ID ADN05275 standard; cDNA; 3719 BP.
 DE Antipsoriatic cDNA sequence #857.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH-) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1458 ID ADM27939 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2004077664-A1.
 PD 22-APR-2004.
 PA (GETH-) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1459 ID ADI95481 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003077659-A1.
 PD 24-APR-2003.
 PA (GETH-) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1460 ID ADI96033 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207354-A1.
 PD 06-NOV-2003.
 PA (GETH-) GENENTECH INC. 21.7%; Score 196.6; DB 13; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1461 ID ADP07205 standard; cDNA; 3963 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 712.
 PN EP2447413-A2.
 PD 18-AUG-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY. 21.7%; Score 196.6; DB 13; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.9e-46;
 RESULT 1462 ID ABA19615 standard; DNA; 4352 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 11946.
 PN WO200152063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. 21.7%; Score 196.6; DB 5; Length 4352;
 Best Local Similarity 81.4%; Pred. No. 1e-45;
 RESULT 1463 ID ACN89730 standard; DNA; 4619 BP.
 DE Breast cancer related marker, seq id 10880.

PN US2003099974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENIUM PHARM INC. 21.7%; Score 196.6; DB 11; Length 4619;
 Best Local Similarity 82.7%; Pred. No. 1e-45;
 RESULT 1464 ID ABX3825 standard; cDNA; 4713 BP.
 DE Human mddt cDNA SEQ ID 386.
 PN WO200279449-A2.
 PD 10-OCT-2002.
 PA (INCY-) INCYTE GENOMICS INC. 21.7%; Score 196.6; DB 8; Length 4713;
 Best Local Similarity 72.4%; Pred. No. 1.1e-45;
 RESULT 1465 ID ACN9177 standard; cDNA; 4823 BP.
 DE Tumour-associated antigenic target (TAT) cDNA DNA325431, SEQ ID NO:3161.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH-) GENENTECH INC. 21.7%; Score 196.6; DB 13; Length 4823;
 Best Local Similarity 72.4%; Pred. No. 1.1e-45;
 RESULT 1466 ID AAK6718 standard; DNA; 5744 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21930.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. 21.7%; Score 196.6; DB 4; Length 5744;
 Best Local Similarity 79.1%; Pred. No. 1.1e-45;
 RESULT 1467 ID AAK66160 standard; DNA; 6153 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20972.
 PN WO200157182-A2.
 PD 05-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. 21.7%; Score 196.6; DB 4; Length 6153;
 Best Local Similarity 82.6%; Pred. No. 1.2e-45;
 RESULT 1468 ID AAK69113 standard; DNA; 10553 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23925.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. 21.7%; Score 196.6; DB 4; Length 10553;
 Best Local Similarity 76.9%; Pred. No. 1.4e-45;
 RESULT 1469 ID ABA16395 standard; DNA; 10553 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 8726.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. 21.7%; Score 196.6; DB 5; Length 10553;
 Best Local Similarity 76.9%; Pred. No. 1.4e-45;
 RESULT 1470 ID AAB14749 standard; DNA; 12394 BP.
 DE Human glycoprotein synthase kinase 3 alpha genomic DNA.
 PN WO200152865-A1.
 PD 26-JUL-2001.
 PA (ISIS-) ISIS PHARM INC. 21.7%; Score 196.6; DB 4; Length 12394;
 Best Local Similarity 80.2%; Pred. No. 1.5e-45;
 RESULT 1471 ID AAV0534 standard; DNA; 14337 BP.
 DE Human cathepsin K gene.
 PN WO20015642-A1.
 PD 18-DEC-1997.
 PA (SMIK-) SMITHKLINE BEECHAM CORP.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (GENO-) INST GENOMIC RBS.
 PA (GENO-) INST GENOMIC RBS. 21.7%; Score 196.6; DB 2; Length 14237;
 Best Local Similarity 81.8%; Pred. No. 1.6e-45;
 RESULT 1472 ID AAL07092 standard; DNA; 14792 BP.
 ID AAL07092 standard; DNA; 14792 BP.

DE Human reproductive system related antigen DNA SEQ ID NO: 9780.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.6; DB 4; Length 14792;
 Best Local Similarity 75.1%; Pred. No. 1.6e-45;
 RESULT 1473
 ID AAV3616 standard; DNA; 15577 BP.
 DE SHOX gene preliminary nucleotide sequence (HOX93).
 PN WO9814568-A1.
 PD 09-APR-1998.
 PA (RAPP-) RAPPOLD-HOERBRAND G. Query Match 21.7%; Score 196.6; DB 2; Length 15577;
 Best Local Similarity 82.6%; Pred. No. 1.7e-45;
 RESULT 1474
 ID AL07093 standard; DNA; 16851 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9781..
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.6; DB 4; Length 16851;
 Best Local Similarity 75.1%; Pred. No. 1.7e-45;
 RESULT 1475
 ID AL07094 standard; DNA; 16853 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9782..
 PN WO200155320-A2.
 PD 02-Aug-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.6; DB 4; Length 16853;
 Best Local Similarity 75.1%; Pred. No. 1.7e-45;
 RESULT 1476
 ID AD50283 standard; DNA; 18099 BP.
 DE Human tumour suppressor gene, Lmt intron 4 DNA.
 PN WO2003066669-A1.
 PD 14-AUG-2003.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA. Query Match 21.7%; Score 196.6; DB 9; Length 18099;
 Best Local Similarity 83.1%; Pred. No. 1.8e-45;
 RESULT 1477
 ID ACM44570 standard; DNA; 19640 BP.
 DE Human genomic sequence hCG38237.
 PN WO2003073026-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY. Query Match 21.7%; Score 196.6; DB 9; Length 19640;
 Best Local Similarity 82.6%; Pred. No. 1.8e-45;
 RESULT 1478
 ID AD5087 standard; DNA; 27184 BP.
 DE Human FOSB carcinoma associated (CA) gene.
 PN WO2003035037-A2.
 PD 01-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY. Query Match 21.7%; Score 196.6; DB 8; Length 27184;
 Best Local Similarity 80.2%; Pred. No. 2.1e-45;
 RESULT 1479
 ID ADA02449 standard; DNA; 27184 BP.
 DE Human FOSB carcinoma associated gene, S8Q ID NO:968.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY. Query Match 21.7%; Score 196.6; DB 9; Length 27184;
 Best Local Similarity 80.2%; Pred. No. 2.1e-45;
 RESULT 1480
 ID ADB72188 standard; DNA; 27184 BP.
 DE Human FOSB gene.
 PN WO2003008838-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY. Query Match 21.7%; Score 196.6; DB 10; Length 27184;
 Best Local Similarity 80.2%; Pred. No. 2.1e-45;
 RESULT 1481
 ID ADE82926 standard; DNA; 27184 BP.
 DE Human FOSB genomic DNA sequence.

PN WO2003080808-A2.
 PD 02-OCT-2003.
 PA (SAGR-) SAGRES DISCOVERY. Query Match 21.7%; Score 196.6; DB 10; Length 27184;
 Best Local Similarity 80.2%; Pred. No. 2.1e-45;
 RESULT 1482
 ID AAV3620 standard; DNA; 32367 BP.
 DE Human SHOX (short stature homeobox containing gene) gene sequence.
 PN WO9814568-A1.
 PD 09-APR-1998.
 PA (RAPP-) RAPPOLD-HOERBRAND G. Query Match 21.7%; Score 196.6; DB 2; Length 32367;
 Best Local Similarity 82.6%; Pred. No. 2.2e-45;
 RESULT 1483
 ID AAK7535 standard; DNA; 38358 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28347.
 PN WO200157102-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC. Query Match 21.7%; Score 196.6; DB 4; Length 38358;
 Best Local Similarity 80.2%; Pred. No. 2.4e-45;
 RESULT 1484
 ID ABQ97152 standard; DNA; 58651 BP.
 DE Human cancer associated sequence HD08-008, SEQ ID 128.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC. Query Match 21.7%; Score 196.6; DB 12; Length 58651;
 Best Local Similarity 82.9%; Pred. No. 2.8e-45;
 RESULT 1485
 ID ADQ9734 standard; DNA; 61739 BP.
 DE Human cancer associated sequence HD08-035, SEQ ID 320.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC. Query Match 21.7%; Score 196.6; DB 12; Length 61739;
 Best Local Similarity 78.1%; Pred. No. 2.8e-45;
 RESULT 1486
 ID AAD39317 standard; DNA; 62804 BP.
 DE Human calcium/calmodulin-dependent protein kinase genomic DNA.
 PN US6387677-B1.
 PD 14-MAY-2002.
 PA (PEKE-) PE CORP NY. Query Match 21.7%; Score 196.6; DB 6; Length 62804;
 Best Local Similarity 70.6%; Pred. No. 2.9e-45;
 RESULT 1487
 ID ABX10916 standard; DNA; 62804 BP.
 DE Genomic DNA encoding novel human kinase.
 PN US200213225-A1.
 PD 19-SEP-2002.
 PA (PEKE-) PE CORP NY. Query Match 21.7%; Score 196.6; DB 8; Length 62804;
 Best Local Similarity 70.6%; Pred. No. 2.9e-45;
 RESULT 1488
 ID AD052582 standard; DNA; 62804 BP.
 DE Human kinase genomic DNA.
 PN US2004101885-A1.
 PD 27-MAY-2004.
 PA (APPL-) APPLERA CORP. Query Match 21.7%; Score 196.6; DB 12; Length 62804;
 Best Local Similarity 70.6%; Pred. No. 2.9e-45;
 RESULT 1489
 ID ACM4594 standard; DNA; 74234 BP.
 DE Human genomic sequence hCG15373.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY. Query Match 21.7%; Score 196.6; DB 11; Length 74234;
 Best Local Similarity 80.2%; Pred. No. 3.1e-45;
 RESULT 1490
 ID ADQ97278 standard; DNA; 86149 BP.
 DE Human cancer associated sequence HD08-025, SEQ ID 254.
 PN WO2004060304-A2.

PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 86149;
 Best Local Similarity 82.6%; Pred. No. 3.2e-45;
 RESULT 1491
 ID ADP08387 standard; DNA; 94400 BP.
 DE Human glycoprotein VI (platelet) (GP6;GPIV;GPVI) genomic DNA.
 Query Match 21.7%; Score 196.6; DB 12; Length 94400;
 Best Local Similarity 82.6%; Pred. No. 3.3e-45;
 RESULT 1492
 ID ADC85367 standard; DNA; 96593 BP.
 DE Mouse Bim coding sequence.
 PN WO200304520-A2.
 PD 05-JUN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 196.6; DB 10; Length 96593;
 Best Local Similarity 80.2%; Pred. No. 3.4e-45;
 RESULT 1493
 ID ADU02888 standard; DNA; 96594 BP.
 DE Human BLM carcinoma associated gene, SEQ ID NO:1406.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 196.6; DB 9; Length 96594;
 Best Local Similarity 80.2%; Pred. No. 3.4e-45;
 RESULT 1494
 ID ADU872626 standard; DNA; 96594 BP.
 DE Human BLM gene.
 PN WO200308583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 196.6; DB 10; Length 96594;
 Best Local Similarity 80.2%; Pred. No. 3.4e-45;
 RESULT 1495
 ID ADM74483 standard; DNA; 96594 BP.
 DE Human carcinoma associated (CA) nucleic acid #76.
 PN US2004072154-A1.
 PD 15-APR-2004.
 PA (MORR/) MORRIS D W.
 PA (ENGE/) ENGEHARD E K.
 Query Match 21.7%; Score 196.6; DB 12; Length 96594;
 Best Local Similarity 80.2%; Pred. No. 3.4e-45;
 RESULT 1496
 ID ADU1740 standard; DNA; 99500 BP.
 DE Human RBCQL2 DNA #1.
 PN US6399378-B1.
 PD 04-JUN-2002.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.7%; Score 196.6; DB 6; Length 99500;
 Best Local Similarity 80.2%; Pred. No. 3.4e-45;
 RESULT 1497
 Query Match 21.7%; Score 196.6; DB 9; Length 110000;
 Best Local Similarity 80.2%; Pred. No. 3.6e-45;
 RESULT 1498
 Query Match 21.7%; Score 196.6; DB 12; Length 110000;
 Best Local Similarity 80.2%; Pred. No. 3.6e-45;
 RESULT 1499
 ID ASN95044 standard; DNA; 110096 BP.
 DE Gene #1542 used to diagnose liver cancer.
 PN WO00223103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 21.7%; Score 196.6; DB 6; Length 110096;
 Best Local Similarity 79.1%; Pred. No. 3.6e-45;
 RESULT 1500
 ID ADU18808 standard; DNA; 111084 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1627.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 111084;
 Best Local Similarity 80.2%; Pred. No. 3.6e-45;

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